(19) World Intellectual Property Organization International Bureau



(43) International Publication Date 10 May 2001 (10.05.2001)

PCT

(10) International Publication Number WO 01/32014 A2

(51) International Patent Classification7:

- (21) International Application Number: PCT/US00/30191
- (22) International Filing Date:

1 November 2000 (01.11.2000)

(25) Filing Language:

English

A01N

(26) Publication Language:

English

- (30) Priority Data:
 - 09/431,705

1 November 1999 (01.11.1999) US

- (71) Applicant: ORAVAX, INC. [US/US]; 38 Sidney Street, Cambridge, MA 02139-4169 (US).
- (72) Inventors: KLEANTHOUS, Harold; 89 Madison Avenue, Newtonville, MA 02160 (US). LONDONO-AR-CILA, Patricia; Flat B, 11 Beckwith Road, London SE24 9LH (GB). FREEMAN, Donna; 68 Thorpe Way, Cambridge CB5 8UB (GB).
- (74) Agent: MICHAUD, Susan, M.; Clark & Elbing LLP, 176 Federal Street, Boston, MA 02110-2214 (US).

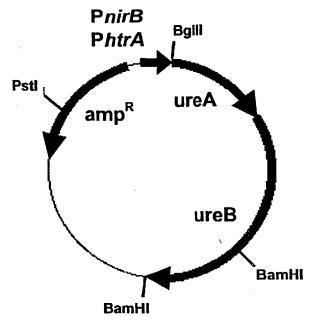
- (81) Designated States (national): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published:

 Without international search report and to be republished upon receipt of that report.

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: USE OF SALMONELLA VECTORS FOR VACCINATION AGAINST HELLICOBACTER INFECTION



(57) Abstract: The invention provides a method of immunization against Helicobacter, involving mucosal administration of an attenuated Salmonella vector including a nucleic acid molecule encoding a Helicobacter antigen, and parenteral administration of a soluble Helicobacter antigen, co-administered with a suitable parenteral adjuvant. Also provided by the invention are attenuated Salmonella vectors for use in this method.



USE OF SALMONELLA VECTORS FOR VACCINATION AGAINST HELICOBACTER INFECTION

5

10

15

20

25

Background of the Invention

This invention relates to the use of Salmonella vectors in vaccination methods against Helicobacter infection.

Helicobacter is a genus of spiral, gram-negative bacteria that colonize the gastrointestinal tracts of mammals. Several species colonize the stomach, most notably *H. pylori*, *H. heilmanii*, *H. felis*, and *H. mustelae*. Although *H. pylori* is the species most commonly associated with human infection, *H. heilmanii* and *H. felis* have also been isolated from humans, but at lower frequencies than *H. pylori*. Helicobacter infects over 50% of adult populations in developed countries and nearly 100% in developing countries and some Pacific rim countries, making it one of the most prevalent infections worldwide.

Helicobacter is routinely recovered from gastric biopsies of humans with histological evidence of gastritis and peptic ulceration. Indeed, *H. pylori* is now recognized as an important pathogen of humans, in that the chronic gastritis it causes is a risk factor for the development of peptic ulcer diseases and gastric carcinoma. It is thus highly desirable to develop safe and effective methods for preventing and treating Helicobacter infection.

Summary of the Invention

The invention provides a method of inducing an immune response against Helicobacter in a mammal. This method involves mucosally (e.g., orally) administering to a mammal (e.g., a human) an attenuated Salmonella (e.g., S. typhi (e.g., CVD908-htrA or CVD908) or S. typhimurium (e.g.,

5

10

15

20

25

BRD509 or BRD807)) vector including a nucleic acid molecule encoding a Helicobacter antigen (e.g., a urease, a urease subunit, or an immunogenic fragment thereof), and parenterally administering to the mammal a Helicobacter antigen (e.g., a urease, a urease subunit, or an immunogenic fragment thereof), optionally, in association with an adjuvant, such as an aluminum compound (e.g., alum). The nucleic acid molecule encoding the Helicobacter antigen can be under the control of a promoter, such as an htrA or a nirB promoter. The antigen used in the mucosal administration can be different from, cross-reactive with, or, preferably, identical to the parenterally administered antigen. In a preferred embodiment, the mucosal administration primes an immune response to an antigen, and the parenteral administration boosts an immune response to the antigen. A mammal treated according to the method of the invention can be at risk of developing, but not have, a Helicobacter infection, or can have a Helicobacter infection. That is, the method can be used to prevent or to treat Helicobacter infection.

The invention also includes use of the Salmonella vectors described above in the preparation of medicaments for preventing or treating Helicobacter (e.g., Helicobacter pylori) infection by mucosal (e.g., oral) administration of the vectors, and parenteral administration of a Helicobacter antigen (e.g., a urease, a urease subunit, or an immunogenic fragment thereof; also see other antigens listed herein), optionally in association with an adjuvant (e.g., alum).

The invention also provides an attenuated Salmonella (e.g., S. typhi (e.g., CVD908-htrA or CVD908) or S. typhimurium (e.g., BRD509 or BRD807)) vector including a nucleic acid molecule encoding a Helicobacter antigen, e.g., a urease, a urease subunit, or an immunogenic fragment thereof, expressed as a fusion protein that can be selectively

targeted to the outer membrane or secreted from the cell. The nucleic acid molecule encoding the Helicobacter antigen can be under the control of a promoter, such as an *htrA* or a *nirB* promoter.

Other features and advantages of the invention will be apparent from the following detailed description, the drawings, and the claims.

Brief Description of the Drawings

Fig. 1 is a schematic representation of an expression plasmid (pH/NUR3) used in Salmonella immunizations.

Fig. 2A is a graph showing the urease-specific serum antibody (IgG2a) response of mice that were mucosally primed with *S. typhimurium*-vectored urease, followed by parenteral boosting with urease and alum.

Fig. 2B is a graph showing the T helper phenotype (IgG1/IgG2a ratio) of mice that were mucosally primed with *S. typhimurium*-vectored urease, followed by parenteral boosting with urease and alum.

Fig. 3A is a graph showing protection against Helicobacter infection in mice that were mucosally primed with *S. typhimurium*-vectored urease, followed by parenteral boosting with urease and alum.

Fig. 3B is a table showing protection against Helicobacter infection in mice that were mucosally primed with *S. typhimurium*-vectored urease, followed by parenteral boosting with urease and alum, as \log_{10} reduction in comparison to a no treatment control group.

Fig. 4 provides the nucleic acid sequence (SEQ ID NOs:1 and 19) and amino acid sequence (SEQ ID NOs:2-18 and 20-30) of plasmid pHUR3.

Fig. 5 is a schematic representation of some relevant features of pHUR3.

20

5

10

15

Detailed Description

This invention provides an immunization method against
Helicobacter infection that involves: (i) mucosal administration of an
attenuated Salmonella vector containing a nucleic acid molecule encoding a
Helicobacter antigen, and (ii) parenteral administration of a Helicobacter
antigen, preferably, in association with an adjuvant. The method can be
used to prevent or to treat Helicobacter infection in a mammal, such as a
human. Also, the mucosal administration can be used to prime an immune
response to an antigen, and the parenteral administration can be used to
boost an immune response to the antigen. The invention also provides
Salmonella vectors for use in this method. Salmonella vectors, Helicobacter
antigens, and adjuvants that can be used in the method of the invention are
first described, as follows. Then, details of the immunization method of the
invention, and examples of its efficacy, are provided.

15 Salmonella Vectors

5

10

20

25

Numerous attenuated Salmonella vectors that can be used in the invention are known in the art, and can be derived from species such as, for example, S. typhi, S. typhimurium, S. enteritidis, S. dublin, S. minnesota, and S. choleraesuis. The vectors can be attenuated chemically (e.g., Ty21a, Swiss Serums and Vaccines, Berna Products) or, preferably, by genetic mutagenesis (e.g., Ty800). For example, attenuation can be achieved by inactivation of key regulatory genes or genes necessary for in vivo survival. For example, the following genes can be inactivated: cya, crp, and asd (cAMP metabolism; see, e.g., Curtiss et al., Vaccine 6:155-160, 1988; Nakayama et al., BioTechnology 6:693, 1988; WO 92/11361), adenylate cyclase and the cAMP receptor (U.S. Patent No. 5,389,368), cdt (invasion of liver and spleen), phoP/phoQ (two component regulator; see, e.g., Fields

et al., Science 243:1059-1062, 1989; U.S. Patent No. 5,424,065), ompR (control of capsule and porin expression; see, e.g., Dorman et al., Infection and Immunity 57:2136-2140, 1989), outer membrane proteins (U.S. Patent No. 5,527,529), reverse mutants of streptomycin mutants (U.S. Patent No. 4,350,684), genes in pathogenicity islands (Shea et al., Infection and Immunity 67:213-219, 1999; WO 99/37759), SPI-2 (invasion of Peyer's patches), Dam (DNA methylation), htrA (heat shock protein; U.S. Patent No. 5,804,194), and other heat shock proteins (U.S. Patent No. 5,804,194). The vectors can also be attenuated by auxotrophic mutations, such as mutations in any of the aroA, aroC, aroD (aromatic compounds), purA, or guaAB (purines) genes (see, e.g., U.S. Patent No. 5,770,214).

5

10

15

. 20

25

Preferably, the mutations in the Salmonella strains used in the invention are non-reverting mutations, *i.e.*, mutations that cannot be repaired in a single step. Mutations of this sort include deletions, inversions, insertions, and substitutions. Preferably, there is more than one mutation in the vector. Methods of making such mutations are well known in the art.

Specific examples of Salmonella vectors that can be used in the invention include *S. typhi* mutant strains, for example, CVD908 *S. typhi* Ty2 ΔατοC/ΔατοD (Hone *et al.*, Vaccine 9:810-816, 1991), CVD908-htrA *S. typhi* Ty2 ΔατοC/ΔατοD/ΔhtrA (Tacket *et al.*, Infection and Immunity 65:452-456, 1997), BRD1116 *S. typhi* Ty2 ΔατοΑ/ΔατοC/ΔhtrA (Lowe *et al.*, Infection and Immunity 67:700-707, 1999), *S. typhi* ΔατοΑ/ΔατοΕ (U.S. Patent No. 5,770,214; deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 12164), *S. typhi* Ty2 ΔατοΑ/ΔατοC Km-R (U.S. Patent No. 5,770,214; deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 12165), and *S. typhi* ΔατοΑ/ΔατοD (U.S. Patent No. 5,770,214;

deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 122309). It has been shown that one of these, CVD908-htrA, is safe and immunogenic in phase I (Tacket *et al.*, Infection and Immunity 65:452-456, 1997) and phase II studies in a total of 100 adult volunteers.

5

10

15

20

25

Specific examples of *S. typhimurium* mutant strains that can be used in the invention include BRD509 *S. typhimurium* ΔaroA/ΔaroD (Strugnell *et al.*, Infection and Immunity 60:3994-4002, 1992), BRD807 *S. typhimurium* ΔaroA/ΔhtrA (Chatfield *et al.*, Microbial Pathogenesis 12:145-151, 1992; U.S. Patent No. 5,804,194; deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 12459), BRD698 (U.S. Patent No. 5,804,194; deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 12457), and BRD726 (U.S. Patent No. 5,804,194; deposited at PHLS, NCTC, 61 Colindale Avenue, London NW9 5HT under Accession No. NCTC 12458).

Additional examples of Salmonella mutant strains that can be used in the invention are described in the following publications: double *aro* mutants (WO 89/05856, U.S. Patent No. 5,770,214), *htrA* mutants (WO 91/15572, U.S. Patent No. 5,804,194), and *ompR* mutants (U.S. Patent No. 5,527,529). Also see, for example, Nakayama *et al.*, BioTechnology 6:693, 1988 and WO 92/11361. In addition, there are numerous alternative strains of *S. typhi* and *S. typhimurium* described in the literature or known in the art that are also attenuated in their virulence, and have been shown to induce immune responses against heterologous antigens. Any of these strains can be used in the method of the present invention.

Any of the attenuated Salmonella strains described above, or others, can be used in the method of the invention to administer a Helicobacter antigen to a mammal for vaccination against Helicobacter infection. This can be accomplished by introducing into the attenuated Salmonella strain a nucleic molecule encoding a Helicobacter antigen. The antigen-encoding nucleic acid molecule to be introduced into the attenuated Salmonella strain can be present, for example, in a plasmid vector (e.g., pHUR3, pHUR4, pNUR3, or pNUR4 (see below)) that includes a regulatory sequence, such as a promoter, and, optionally, a sequence encoding a secretion signal (e.g., a bacterial hemolysin (hly) secretion signal; WO 87/06953, U.S. Patent No. 5,143,830).

The promoter can be a prokaryotic promoter, for example, a Salmonella promoter, which directs expression of the Helicobacter antigen in the Salmonella vector. Examples of such promoters include the *htrA* promoter (WO 95/20665), the *nirB* promoter (WO 92/15689, U.S. Patent No. 5,547,664), the *ssaH* promoter (Valdivia *et al.*, Science 277:2007-2011, 1997), the *ompR* promoter, and any other Salmonella or other bacterial promoter that is upregulated when Salmonella is taken up by mammalian cells. Alternatively, the promoter can be a eukaryotic promoter, such as the cytomegalovirus promoter. Use of such promoters allows for expression of target antigen in a eukaryotic cell, with Salmonella acting as the delivery vehicle for this DNA immunization approach. The construction of such vectors is known in the art. Of course, numerous eukaryotic promoters are known in the art and can be used in the invention.

25

5

10

15

20

Introduction of a plasmid into an attenuated Salmonella strain can be accomplished using any of a number of standard methods, such as electroporation or bacteriophage transduction (Turner *et al.*, Infection and Immunity 61:5374-5380, 1993). Also see, *e.g.*, Ausubel *et al.*, *Current*

Protocols in Molecular Biology, John Wiley & Sons Inc., 1994, and Ward et al., Infection and Immunity 67(5):2145-2152, 1999, for methods of introducing plasmids into bacteria, such as Salmonella.

Helicobacter Antigens

5

10

15

20

25

Preferred antigens for use in the invention are Helicobacter (e.g., H. pylori or H. felis) proteins (i.e., peptides or polypeptides), other components Helicobacter (e.g., lipopolysaccharides, carbohydrates, or nucleic acid molecules), or immunogenic fragments thereof. Preferably, the same or a similar (e.g., a fragment) antigen is used in the mucosal administration step as in the parenteral administration step, however, the antigen used in each of these steps can differ. Also, preferably, the mucosally administered antigen primes an immune response to the antigen, and the parenterally administered antigen boosts an immune response to the same antigen. For the mucosal administration step, a nucleic acid molecule (e.g., a DNA molecule) encoding a desired antigen is inserted into an attenuated Salmonella vector, as is described above. For the parenteral administration step, the antigen can be, for example, purified from a bacterial culture or produced using standard recombinant or chemical synthetic methods. Methods for identifying immunogenic fragments of polypeptide antigens are known in the art, and can be employed in preparing antigens for use in the method of the invention (see, e.g., Sturniolo et al., Nature Biotechnology, "Generation of Tissue-Specific and Promiscuous HLA Ligand Databases Using DNA Microarrays and Virtual HLA Class II Matrices," June, 1999). Additional antigens that can be used in the parenteral administration step are whole Helicobacter bacteria and nonpurified protein preparations, such as Helicobacter lysates.

5

10

15

20

25

The antigens used in the invention can be produced as fusion proteins, which are polypeptides containing amino acid sequences corresponding to two or more proteins (or fragments thereof) that are normally separate proteins, linked together by a peptide bond(s). Fusion proteins generally are synthesized by expression of a hybrid gene, containing nucleotides encoding each of the individual polypeptides that make up the fusion protein. An example of an antigenic fusion protein that can be used in the invention is one that contains a cholera toxin (CT) or an E. coli heat-labile toxin (LT) adjuvant (e.g., a toxin A or B subunit, or a fragment or derivative thereof having adjuvant activity) fused to an H. pylori antigen, e.g., a urease antigen. Another type of fusion protein included in the invention consists of an antigen fused to a polypeptide (e.g., glutathione S-transferase (GST)) that facilitates purification of the fusion protein. Still another type of fusion protein that can be used in the invention is a fusion with a polypeptide that targets the expressed protein to cells of the immune system. For example, fusions with CD4 or Staph A can be used. Proteins used as antigens in the invention can also be covalently coupled or chemically cross-linked to adjuvants, using standard methods.

The most preferred *H. pylori* antigens for use in the invention are urease antigens, which include, *e.g.*, immunogenic fragments or subunits (*e.g.*, UreA or UreB) of urease. Most preferred urease antigens are enzymatically inactive, recombinant multimeric urease complexes, produced as described in Lee *et al.*, WO 96/33732. A number of other immunogenic *H. pylori* antigens can be administered according to the invention, *e.g.*, catalase (WO 95/27506), HspA and HspB (WO 94/26901), lactoferrin receptor (WO 97/13784), p76 (WO 97/12908), p32 (WO 97/12909), BabA and BabB (WO 97/47646), AlpA (WO 96/41880), AlpB (WO 97/1182), as well as the antigens described in WO 96/38475, WO

96/40893, WO 97/19098, WO 97/37044, WO 98/18323, WO 97/37044, WO 97/4764, WO 98/04702, and WO 98/32768. Additional preferred antigens for use in the invention are GHPO 1516, GHPO 789, GHPO 386, GHPO 1615, GHPO 1360, GHPO 1320, GHPO 639, GHPO 792, GHPO 536, GHPO 525, GHPO 1275, GHPO 1688, GHPO 706, GHPO 419, GHPO 1595, GHPO 1398, GHPO 986, GHPO 1282, GHPO 1056, GHPO 1443, GHPO 13, GHPO 109, GHPO 257, GHPO 1034, GHPO 236, GHPO 1166, GHPO 1351, and GHPO 1420 (WO 98/21225, WO 98/43478, and WO 98/43479), as well as other antigens described in these publications.

10 Adjuvants

5

15

20

25

Although not required, the attenuated Salmonella vectors described above for mucosal administration step can be administered with a mucosal adjuvant. The adjuvant can be admixed with the Salmonella vector or expressed in the Salmonella vector (e.g., as a fusion protein with an antigen, see above), either from an integrated nucleic acid molecule or episomally, e.g., on a plasmid. Such adjuvants can be chosen from bacterial toxins, e.g., the cholera toxin (CT), the E. coli heat-labile toxin (LT), the Clostridium difficile toxin, and the Pertussis toxin (PT), or combinations, subunits, toxoids, fragments, homologs, derivatives, fusions, or mutants that are derived therefrom and have adjuvant activity. For example, it is possible to use a purified preparation of the native cholera toxin B subunit (CTB) or a polypeptide including the carboxyl-terminal repeats of C. difficile toxin A (WO 97/02836). Preferably, a mutant is used in which toxicity is reduced. Such mutants are described in, e.g., WO 95/17211 (mutant CT Arg-7-Lys), WO 96/6627 (mutant LT Arg-192-Gly), and WO 95/34323 (mutant PT Arg-9-Lys and Glu-129-Gly). Other LT mutants that can be used include at least one of the following mutations: Ser-63-Lys, Ala-69-Gly,

Glu-110-Asp, and Glu-112-Asp. Other compounds, such as MPLA, PLGA, and QS-21, can also be used as adjuvants for the mucosal route.

Adjuvants for use in parenteral administration include, for example, aluminum compounds (e.g., alum), such as aluminum hydroxide, aluminum phosphate, and aluminum hydroxy phosphate. The antigen can be precipitated with, or adsorbed onto, the aluminum compound using standard methods.

5

10

15

20

25

In addition to aluminum compounds, a large number of appropriate adjuvants for administration by the systemic or parenteral route exist in the art and can be used in the invention. For example, liposomes; ISCOMS; microspheres; protein chochleates; vesicles consisting of nonionic surfactants; cationic amphiphilic dispersions in water; oil/water emulsions; muramidyldipeptide (MDP) and its derivatives, such as glucosyl muramidyldipeptide (GMDP), threonyl-MDP, murametide, and murapalmitin; QuilA and its subfractions; as well as various other compounds, such as DC-chol; monophosphoryl-lipid A (MPLA) major lipopolysaccharide from the wall of a bacterium, for example, *E. coli*, *S. minnesota*, *S. typhimurium*, *Shigella flexneri*, or *N. meningitidus*; alganglucan; gamma-inulin; calcitriol; and loxoribine can be used. Other adjuvants, such as RIBI (ImmunoChem, Hamilton, MT) and polyphosphazene (WO 95/2415), can also be used in parenteral administration.

Useful liposomes for the purposes of the present invention can be selected, for example, from pH-sensitive liposomes, such as those formed by mixing cholesterol hemisuccinate (CHEMS) and dioleyl phosphatidyl ethanolamine (DOPE); liposomes containing cationic lipids recognized for their fusiogenic properties, such as 3-beta-(N-(N',N'-dimethylamino-ethane)carbamoyl)cholesterol (DC-chol) and its equivalents, which are

described in U.S. Patent No. 5,283,185 and WO 96/14831; dimethyldioctadecylammonium bromide (DDAB) and the BAY compounds described in EP 91645 and EP 206 037, for example, Bay R1005 (N-(2-deoxy-2-L-leucylamino-beta-D-glucopyranosyl)-N-octa-decyldodecanoylamide acetate; and liposomes containing MTP-PE, a lipophilic derivative of MDP (muramidyldipeptide). These liposomes are useful as adjuvants with all of the antigens described herein.

5

10

15

20

25

Useful ISCOMs for the purposes of the present invention can be selected, for example, from those compounds of QuilA or of QS-21 combined with cholesterol and, optionally, also with a phospholipid, such as phosphatidylcholine. These are particularly advantageous for the formulation of the lipid-containing antigens.

Useful microspheres for the purposes of the present invention can be formed, for example, from compounds such as polylactide-co-glycolide (PLAGA), alginate, chitosan, polyphosphazene, and numerous other polymers.

Useful protein chochleates for the purposes of the present invention can be selected, for example, from those formed from cholesterol and, optionally, an additional phospholipid, such as phosphatidylcholine. These are especially advantageous for the formulation of the lipid-containing antigens.

Useful vesicles consisting of nonionic surfactants for the purposes of the present invention can be, for example, formed by a mixture of 1-monopalmitoyl glycerol, cholesterol, and dicetylphosphate. They are an alternative to conventional liposomes, and can be used for the formulation of all of the antigens described herein.

Useful oil/water emulsions for the purposes of the present invention can be selected, for example, from MF59 (Biocine-Chiron), SAF1 (Syntex), and the montanides ISA51 and ISA720 (Seppic).

A useful adjuvant for the purposes of the present invention can also be a fraction derived from the bark of the South American tree *Quillaja Saponaria Molina*, for example, QS-21, a fraction purified by HPLC chromatography as is described in U.S. Patent No. 5,057,540. Since some toxicity may be associated with QS-21, it may be advantageous to use it in liposomes based on sterol, as is described in WO 96/33739.

Induction of an Immune Response Against Helicobacter

5

10

15

20

25

The method of the invention can be used to prevent Helicobacter infection in a patient, as well as to treat an ongoing Helicobacter infection in a patient. Thus, gastroduodenal diseases associated with these infections, including acute, chronic, or atrophic gastritis, and peptic ulcers, e.g., gastric or duodenal ulcers, can be prevented or treated using the method of the invention.

As is noted above, the method of the invention involves mucosal (e.g., oral, intranasal, intragastric, pulmonary, intestinal, rectal, ocular, vaginal, or urinary tract) administration of a Salmonella vector including a nucleic acid molecule that encodes a Helicobacter antigen, followed by parenteral (e.g., intramuscular, subcutaneous, intradermal, intraepidermal, intravenous, or intraperitoneal) administration of a Helicobacter antigen, preferably in association with an adjuvant. The antigen used in the mucosal prime can be different from, cross-reactive with, or, preferably, identical to the parenterally administered antigen. Preferably, the mucosal administration step primes an immune response to an antigen, and the parenteral administration step boosts an immune response to the antigen.

Also included in the invention are vaccination methods involving parenteral priming and mucosal boosting (e.g., with a Salmonella vector including a nucleic acid molecule encoding a Helicobacter antigen), and parenteral administration of a Salmonella vector including a nucleic acid molecule encoding a Helicobacter antigen.

5

10

15

20

25

Attenuated Salmonella vectors, antigens, formulations, adjuvants, administration regimens, specific mucosal and parenteral routes, and dosages to be used in the method of the invention can readily be determined by one skilled in the art. For example, 5 x 10⁶ - 5 x 10¹⁰ colony forming units, e.g., 5 x 10⁸ colony forming units, of an attenuated Salmonella vector can be used in the mucosal administration, and 5-1000 μg, e.g., 100 μg, antigen, can be used in the parenteral administration. The mucosal administration can take place only once or two or more (e.g., three, four, or five) times, for example, separated by two, three, or four days or weeks. Similarly, the parenteral administration can take place once or two or more (e.g., three, four, or five) times, separated by weeks, months, or years from each other or the mucosal administration.

In one example of an immunization regimen that can be used, a patient is primed with two doses of an attenuated Salmonella vector (e.g., S. typhi CVD908-htrA or CVD908, or S. typhimurium BRD509 or BRD807) expressing an antigen (e.g., urease from plasmid pHUR3, pHUR4, pNUR3, or pNUR4) on days 0 and 21, and then parenterally boosted on day 51 or later with an antigen (e.g., urease) and an adjuvant (e.g., alum). The details of construction of pHUR3 and pNUR3, which each include an ampicillin resistance gene, are described below. pHUR4 and pNUR4 are constructed by removing the ampicillin resistance gene from pHUR3 and pNUR3, respectively, by digestion with the restriction endonuclease RcaI, and

cloning into the digested vectors a kanamycin resistance gene that can be obtained from plasmid pUC4K (Pharmacia) by digestion with *EcoRI*.

A useful pharmaceutical composition for the purposes of the present invention can be manufactured in a conventional manner. In particular, it can be formulated with a pharmaceutically acceptable carrier or diluent, e.g., water or a saline solution. In general, the diluent or carrier can be selected according to the mode and route of administration and according to standard pharmaceutical practices. Appropriate carriers or diluents, as well as what is essential for the preparation of a pharmaceutical composition, are described, e.g., in Remington's Pharmaceutical Sciences (18th edition), ed. A. Gennaro, 1990, Mack Publishing Company, Easton, PA., a standard reference book in this field. As a specific example, the attenuated Salmonella vectors of the invention can be formulated in a tablet for oral administration (see, e.g., U.S. Patent No. 5,804,194).

15

20

25

10

5

The therapeutic or prophylactic efficacy of the method of the invention can be evaluated according to standard methods, e.g., by measuring the induction of an immune response or the induction of therapeutic or protective immunity using, e.g., the mouse/H. felis model and the procedures described in Lee et al., Eur. J. Gastroenterology and Hepatology 7:303, 1995 or Lee et al., J. Infect. Dis. 172:161, 1995. Persons skilled in this art will realize that H. felis can be replaced in the mouse model by another Helicobacter species. For example, the efficacy of the method is, preferably, evaluated in a mouse model using an H. pylori strain adapted to mice. The efficacy can be determined by comparing the level of infection in gastric tissue (e.g., by measuring the urease activity, bacterial load, or condition of the gastritis) with that in a control group. A therapeutic effect or a protective effect exists when infection is reduced

compared with a control group. Experimental methods and results showing the efficacy of the present method is described as follows.

Experimental methods and results

Construction of ureAB expression plasmids under the control of the nirB and htrA promoters - Method 1

A ureAB expression plasmid is constructed by subcloning a PCR product containing the ureAB genes (amplified from plasmid pORV273) into plasmid vector ptetnir15. Plasmid pORV273 is obtained from OraVax, Inc., Cambridge, MA. Plasmid ptetnir15 has been described (Chatfield et al., Bio/Technology 10:888-892, 1992; Oxer et al., Nucl. Acids Res. 19:1889-1892, 1991). This vector was modified by standard techniques known in the art, to introduce into the vector a suitable restriction site for subcloning other genes for optimal expression under control of the nirB promoter. An Ncol site was introduced 10 basepairs 3' to the Shine-Dalgarno sequence of ptetnir15, and the resultant plasmid is designated ptetnir15/mod. Plasmid ptetnir15/mod, carried in strain BRD940, is obtained from Peptide Therapeutics Ltd., Cambridge, U.K.

The *ureAB* gene is amplified by PCR from pORV273 using Turbo Pfu polymerase (Stratagene), which has 3'-5' proof-reading activity, and two primers, designated orafor and orarev. Primer orafor introduces *Eco*RI and *Bsp*HI sites immediately upstream of the initiating codon of the *ureA* gene. Primer orarev binds approximately 18 basepairs downstream of the *Bam*HI site that is located 45 basepairs downstream of the termination codon of the *ureB* gene.

The PCR reaction includes 0.1 µg pORV273 and 100 pmol each of primers orafor (5'-TAG GGA ATT CTC ATG AAA CTC ACC CCA AAA G-3' (SEO ID NO:31)) and orarev (5'-GCC AAC TTA GCT TCC TTT

5

10

15

20

CGG G-3' (SEQ ID NO:32)) per 100 µl reaction and utilizes 25 cycles, with an annealing temperature of 50°C. The resulting 2.4 kb PCR product is purified from a 1% agarose gel using a Qiaquick gel extraction kit (Qiagen). As is described below, the actual method used in the generation of pNUR and pHUR differed from this description in the sequence of orarev. Therefore, the method described here may need to be adapted in ways known to those skilled in the art by changing, for example, the precise annealing temperature or the number of cycles required to give sufficient product, or even in the sequence of the primer orarev.

10

5

The PCR product is digested with *BspHI + BamHI*, and purified with a Promega Wizard DNA clean-up kit. Plasmid ptetnir15/mod is digested with *NcoI + BamHI* (the *NcoI* site is 10 basepairs 3' to the Shine-Dalgarno sequence of ptetnir15, and generates a cohesive end that is compatible with *BspHI*), and dephosphorylated using shrimp alkaline phosphatase. The largest fragment from the digestion of ptetnir15/mod is isolated from a 1% agarose gel using a Qiaquick gel extraction kit (Qiagen), and ligated to the digested PCR product using the Ligator Express Kit (Clontech). Ligations are transformed into electrocompetent *E. coli* TG1 cells (Stratagene).

20

15

Plasmids from ampicillin-resistant transformants are screened for the presence of the full length, 2.4 kb ureAB gene by restriction analysis. The ureAB gene from plasmid pORV273 has a BamHI site within the coding sequence. However, in a small number of ptetnir15/mod + ureAB transformants, incomplete digestion or re-ligation of the two ureAB fragments yields the full length ureAB PCR product. The orientation of the ureAB gene in the ptetnir15-derived plasmid is confirmed by PCR, and a plasmid with the full length ureAB gene, in the correct orientation is designated pNUR.

25

The *nirB* promoter in plasmid pNUR is replaced with the *htrA* promoter from phtrAcore, which is obtained from Peptide Therapeutics Ltd., Cambridge, U.K. Plasmids pNUR and phtrAcore are digested with *PstI* and *BgIII*. Digested pNUR is dephosphorylated with shrimp alkaline phosphatase. The digestion products are run on a 1% agarose gel, and a 0.8 kb fragment containing the *htrA* promoter from the phtrAcore digestion and the 4.0 kb fragment from pNUR lacking the *nirB* promoter are extracted from the gel using a Qiagen Qiaquick gel extraction kit. The two fragments are ligated together (Clontech Ligator express kit), and transformed into electrocompetent *E. coli* TG1 cells (Stratagene). Transformants are screened for the presence of the *htrA* promoter by PCR using primer pairs specific for *htrA* (5902/5904) or *nirB* (5901/5904). A plasmid with the *htrA* promoter and a full length *ureAB* gene is designated pHUR.

5

10

15

20

25

The nucleotide sequence across the promoter region and *ureAB* genes of final plasmids are confirmed. Samples of the plasmids are prepared using the Qiagen "Plasmid midi kit" (Catalog No. 12143), and the DNA sequence determined by standard techniques. Oligonucleotides 5901 to 5919 (see below) can be used, and allow nucleotide sequence determination of both DNA strands. Oligonucleotides 5901 and 5902 hybridize within *nirB* and *htrA*, respectively, while 5919 hybridizes within ptetnir15/mod, downstream of the *ureAB* genes. The other oligonucleotides hybridize within the *ureAB* genes. The data confirm that the nucleotide sequence across the recombinant region of all plasmids are as expected.

Plasmids pNUR and pHUR are introduced into *S. typhimurium* strains such as, *e.g.*, BRD509 and BRD807, and *S. typhi* strains such as, *e.g.*, CVD908 and BRD948, by electroporation and selection of ampicillinresistant colonies.

Construction of ureAB expression plasmids under the control of the nirB and htrA promoters - Method 2

5

10

15

20

25

The protocol described above is one example of many by which one skilled in the art can derive an expression plasmid suitable for directing the synthesis of an H. pylori antigen, e.g., urease, under the control of the htrA or nirB promoter in an attenuated strain of Salmonella. Alternative primers can be used in the PCR amplification of the genes from the starting plasmid, and alternative strategies for the introduction of the gene via alternative restriction sites are possible. One such alternative was employed in the construction of plasmids pNUR3 and pHUR3. During the design of the primers for PCR, a sequence error in the database-deposited gene sequence caused the 3' end of the ureB gene to be incorrectly identified. A primer was synthesized for the PCR amplification that, in fact, resulted in a non-native sequence of the gene, containing an additional 49 codons after the genuine termination codon. This error was subsequently corrected by the method described below, yielding a final plasmid with a sequence identical to that of the plasmid that would be produced by the strategy described above. This method is described in further detail, as follows.

As is described above, plasmid pORV273 was obtained from OraVax Inc. Plasmid ptetnir15 has been described (Chatfield *et al.*, Bio/Technology 10:888-892, 1992; Oxer *et al.*, Nucl. Acids Res. 19:1889-1892, 1991), and this vector was modified by standard techniques, to introduce into the vector a suitable restriction site for subcloning other genes for optimal expression under control of the *nirB* promoter. An *Nco*I site was introduced 10 basepairs 3' to the Shine-Dalgarno sequence of ptetnir15, and the resultant plasmid was designated ptetnir15/mod. Plasmid ptetnir15/mod, carried in strain BRD940, was obtained from the culture collection of Peptide Therapeutics Ltd., Cambridge, U.K.

The ureAB gene was amplified by PCR from pORV273 using Turbo Pfu polymerase (Stratagene), which has 3'-5' proof-reading activity and two primers, designated orafor and orarev. Primer orafor introduces *EcoRI* and *BspHI* sites immediately upstream of the initiating codon of the *ureA* gene. Primer orarev introduces a *BamHI* and a *PstI* site just before the correct 3' end of the *ureAB* gene. Subsequent digestion and cloning, as is described below, resulted in the deletion of the correct termination codon of *ureB*, with the result that transcription continued into the vector sequence until an in-frame stop codon was reached, adding 49 amino acids to the translated protein.

5

10

15

20

25

The PCR reaction included 0.1 µg pORV273 and 100 pmol each of primers orafor (5'-TAG GGA ATT CTC ATG AAA CTC ACC CCA AAA G-3' (SEQ ID NO:31)) and orarev (5'-TCT ACT GCA GGA TCC AAA ATG CTA AAG AGT TGC G-3' (SEQ ID NO:33)) per 100 µl reaction, and utilized 25 cycles, with an annealing temperature of 50°C. The resulting 2.4 kb PCR product was purified from a 1% agarose gel using a Qiaquick gel extraction kit (Qiagen). The PCR product was digested with BspHI + BamHI, and purified with a Promega Wizard DNA clean-up kit. Plasmid ptetnir15/mod was digested with NcoI + BamHI (the NcoI site is 10 basepairs 3' to the Shine-Dalgarno sequence of ptetnir15, and generates a cohesive end that is compatible with BspHI), and dephosphorylated using shrimp alkaline phosphatase. The largest fragment from the digestion of ptetnir15/mod was isolated from a 1% agarose gel using a Qiaquick gel extraction kit (Qiagen), and ligated to the digested PCR product using the Ligator Express Kit (Clontech). Ligations were transformed into electrocompetent E. coli TG1 cells (Stratagene).

Plasmids from ampicillin-resistant transformants were screened for the presence of the full length, 2.4 kb *ureAB* gene by restriction analysis. The *ureAB* gene from plasmid pORV273 has a *BamHI* site within the coding sequence. However, in a small number of ptetnir15/mod + *ureAB* transformants, incomplete digestion or re-ligation of the two *ureAB* fragments yielded the full length *ureAB* PCR product. The orientation of the *ureAB* gene in the ptetnir15-derived plasmid was confirmed by PCR and a plasmid with the full length *ureAB* gene, in the correct orientation was designated pNUR1.

10

15

5

The *nirB* promoter in plasmid pNUR1 was replaced with the *htrA* promoter from phtrAcore, which is obtained from Peptide Therapeutics Ltd., Cambridge, U.K. Plasmids pNUR1 and phtrAcore were digested with *Pst*I and *BgI*II. Digested pNUR1 was dephosphorylated with shrimp alkaline phosphatase. The digests were run on a 1% agarose gel, and a 0.8 kb fragment containing the *htrA* promoter from the phtrAcore digest and the 4.0 kb fragment from pNUR1 lacking the *nirB* promoter were extracted from the gel using a Qiagen Qiaquick gel extraction kit. The two fragments were ligated together (Clontech Ligator express kit) and transformed into electrocompetent *E. coli* TG1 cells (Stratagene). Transformants were screened for the presence of the *htrA* promoter by PCR using primer pairs specific for *htrA* (5902/5904) or *nirB* (5901/5904). A plasmid with the *htrA* promoter and a full length *ureAB* gene was designated pHUR1.

20

25

Subsequent to this it was discovered that there had been a cloning error in the 3' terminal portion of *ureB*, resulting in a translated product with an additional 49 amino acids from both pHUR1 and pNUR1. This was corrected by replacing the small *Bam*HI fragment containing the C-terminus of the *ureB* gene with the corresponding, and correct, fragment from pORV272. pORV273, pHUR1, and pNUR1 were digested with *Bam*HI,

and the small fragment from the pORV273 digestion was ligated to the large fragment from the pHUR1 and pNUR1 digestions. Clones were screened for orientation of the insert, and clones with the correct orientation were designated pHUR3 and pNUR3. These clones were characterized by full nucleotide sequencing of the region including the promoter and the complete *ureAB* gene on both strands, and found to be correct.

The nucleotide sequences across the *nirB* promoter and *ureAB* genes of pNUR1 and of the *htrA* promoter region of pHUR1 were confirmed. Samples of the two plasmids were prepared using the Qiagen "Plasmid midi kit" (Catalogue No. 12143), and the DNA sequence was determined by standard techniques known in the art. Oligonucleotides 5901 to 5919 were used, which allow nucleotide sequence determination of both DNA strands. Oligonucleotides 5901 and 5902 hybridize within *nirB* and *htrA*, respectively, while 5919 hybridizes within ptetnir15/mod downstream of the *ureAB* genes. The other oligonucleotides hybridize within the *ureAB* genes. These were diluted to 1 pmol µl⁻¹, packed in dry ice with the plasmid samples, and sent to Cambridge Bioscience (Cambridge) for nucleotide sequence determination. The data confirmed that the nucleotide sequence across the recombinant region of all three plasmids was as expected.

Sequences of primers that can be used in the invention, as is described above, are as follows.

5901

5

10

15

20

Primes within *nirB* promoter ~60 basepairs upstream of SD sequence TCA AAT GGT ACC CCT TGC TGA (SEQ ID NO:34)

25 5902 Primes within htrA promoter ~60 basepairs upstream of SD sequence TAT TCC GGA ACT TCG CGT TA (SEQ ID NO:35)

5903

Primes ~250 basepairs downstream from start of *ureA* gene TGT TTC CTG ATG GGA CTA AAC TC (SEQ ID NO:36)

5904

5 Reverse primes ~300 basepairs downstream from start of *ureA* gene ACC AGG AAC TAA TTT ACC ATT G (SEQ ID NO:37)

5905

Primes ~550 basepairs downstream from start of *ureA* gene TTG ATT GAC ATT GGC GGT AAC (SEQ ID NO:38)

10 5906

Reverse primes ~600 basepairs from start of *ureA* gene GTT GTC TGC TTG TCT ATC AAC C (SEQ ID NO:39)

5907

Primes ~150 basepairs downstream from start of *ureB* gene GGT GGC GGT AAA ACC CTA AGA G (SEQ ID NO:40)

5908

Reverse primes ~180 basepairs downstream of *ureB* gene CTT TGC TAG GGT TGT TAG ATT G (SEQ ID NO:41)

5909

20 Primes ~400 basepairs downstream from start of *ureB* gene AAT CCC TAC AGC TTT TGC AAG C (SEQ ID NO:42)

5910

Reverse primes ~500 basepairs from start of *ureB* gene GTG CCA TCA GCA GGA CCG GTT C (SEQ ID NO:43)

25 5911

30

Primes ~750 basepairs from start of *ureB* gene ATC GCC ACA GAC ACT TTG AAT G (SEQ ID NO:44)

5912

Reverse primes ~820 basepairs downstream from start of *ureB* gene TAG CAG CCA TAG TGT CTT CTA C (SEQ ID NO:45)

5913

Primes ~1050 basepairs downstream from start of *ureB* gene TGA AGA CAC TTT GCA TGA CAT G (SEQ ID NO:46)

5914

5 Reverse primes 1080 basepairs downstream of *ureB* gene TGA GAG TCA GAA CTG GTG ATT G (SEQ ID NO:47)

5915

Primes ~1350 basepairs downstream from start of *ureB* gene CAT GAT CAA AGG CGG ATT C (SEQ ID NO:48)

10 5916

15

Reverse primes ~1380 basepairs downstream from start of *ureB* GAA GCG TTC GCA TCG CCC ATT TG (SEQ ID NO:49)

5917

Primes ~1650 basepairs from start of *ureB*TCG TGG ATG GCA AAG AAG TAA C (SEQ ID NO:50)

5918

Reverse primes ~1680 basepairs from start of *ureB* GCG CCA AGC TCA CTT TAT TG (SEQ ID NO:51)

5919

20 Reverse primes ~80 basepairs downstream of *Bam*HI site downstream of *ureB*CAA CGA CAG GAG CAC GAT CAT G (SEQ ID NO:52)

The nucleotide sequences across the promoter regions and *ureAB* genes of the final plasmids, pHUR3 and pNUR3, were also confirmed. *E. coli* MC1061 cells containing the plasmids were sent to Cambridge Biosciences Ltd., who prepared plasmid DNA and determined the nucleotide sequences of the promoter and *ureAB* genes of both plasmids. The data confirmed that the nucleotide sequence across the relevant region of both plasmids was as expected. The sequence of plasmid pHUR3 is

shown in Fig. 4, and a plasmid map showing its relevant features is provided in Fig. 5.

Plasmids pNUR and pHUR were introduced into *S. typhimurium* strains BRD509 and BRD807, and *S. typhi* strains CVD908 and BRD948, by electroporation and selection of ampicillin-resistant colonies.

Immunization and Protection Experiments

5

10

15

20

25

Inbred Balb/C mice were immunized by the intragastric route with live, attenuated Salmonella typhimurium (1E10 CFU/ml) expressing urease apoenzyme on day 0 (Fig. 1). Animals were boosted twice on days 21 and 35 with 10 µg soluble, recombinant urease plus aluminum hydroxide (200 ug) by the parenteral route. Fourteen days later, serum antibody responses to urease were measured. Controls included: (1) prime-boost with the Salmonella parental control strains (BRD509 ΔaroA/ΔaroD (Strugnell et al., Infection and Immunity 60:3994-4002, 1992) and BRD807ΔaroA/ΔhtrA (Chatfield et al., Microbial Pathogenesis 12:145-151, 1992)) minus the urease construct, (2) mucosal priming with LT in place of Salmonella (gold standard), and (3) parenteral immunization with urease plus alum alone. Attenuated S. typhimurium ($\Delta \text{aroA}/\Delta \text{aroD}$) expressing urease under the transcriptional control of either an htrA promoter (pHUR3) or the nirB promoter (pNUR3) induced an elevated IgG2a response against urease that was greater than the gold standard using LT-Alum (Fig. 2A). A comparable response to LT-Alum was induced with S. typhimurium (ΔaroA/ΔhtrA) carrying the same urease constructs (Fig. 2A). Analysis of the IgG1/IgG2a ratio demonstrated the induction of a Th1 response with the double aro mutant, and a more balanced response with the $\Delta aro/\Delta htrA$ mutant strain (Fig. 2B). Urease-specific antibody in Fig. 2A is expressed as EU/ml on a logarithmic scale and median response is indicated by the bar.

The level of protective efficacy employing *S. typhimurium*-vectored urease in a prime-boost strategy was determined. Fig. 3A shows the results of quantitative *H. pylori* culture of mice immunized on day 0 with 1E10 CFU/ml live attenuated *S. typhimurium* (ΔaroA/ΔaroD or ΔaroA/ΔhtrA) and boosted on days 21 and 35 with urease (10 μg) plus alum (200 μg). Three weeks later, animals were challenged with *H. pylori* (1E7 CFU/ml) and efficacy was assessed in gastric tissue 4 weeks later using quantitative culture. Strains including the urease constructs are indicated in the key of Fig. 3A. Fig. 3B shows protection depicted as log₁₀ reduction in comparison to the no treatment (Tx) control group. A significant reduction in bacterial burden was observed when attenuated Salmonella expressing urease was administered as part of a prime-boost regimen with alum (Wilcoxon rank sum compared to parental control strain). No significant difference was observed between group 1 (pHUR3-Alum) and group 7 (LT-Alum).

All patents and publications cited above are hereby incorporated by reference in their entirety.

What is claimed is:

5

10

15

1. A method of inducing an immune response against Helicobacter in a mammal, said method comprising the steps of:

mucosally administering to said mammal an attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen, and

5

10

parenterally administering to said mammal a Helicobacter antigen.

- 2. The method of claim 1, wherein said attenuated Salmonella vector is administered orally to said mammal.
- 3. The method of claim 1, wherein said Helicobacter antigen is a urease, a urease subunit, or an immunogenic fragment thereof
 - 4. The method of claim 1, wherein said mammal is at risk of developing, but does not have, a Helicobacter infection.
 - 5. The method of claim 1, wherein said mammal has a Helicobacter infection.
- 6. The method of claim 1, wherein said parenteral administration of said Helicobacter antigen further includes parenteral administration of an adjuvant.
 - 7. The method of claim 6, wherein said adjuvant is an aluminum compound.
- 8. The method of claim 7, wherein said aluminum compound is alum.

9. The method of claim 1, wherein said attenuated Salmonella vector is a Salmonella typhi vector.

- 10. The method of claim 9, wherein said *Salmonella typhi* vector is CVD908-htrA or CVD908.
- 5 11. The method of claim 1, wherein the attenuated Salmonella vector is a Salmonella typhimurium vector.
 - 12. The method of claim 11, wherein said *Salmonella typhimurium* vector is BRD509 or BRD807.
- 13. The method of claim 1, wherein said attenuated Salmonella
 vector further comprises an htrA promoter.
 - 14. The method of claim 1, wherein said attenuated Salmonella vector further comprises a *nirB* promoter.
 - 15. The method of claim 1, wherein said mucosal administration primes an immune response to an antigen and said parenteral administration boosts an immune response to said antigen.

15

- 16. An attenuated Salmonella vector comprising a nucleic acid molecule encoding a Helicobacter antigen.
- 17. The vector of claim 16, wherein said antigen is a urease, a urease subunit, or an immunogenic fragment thereof.

18. The vector of claim 16, wherein said attenuated Salmonella vector is a *Salmonella typhi* vector.

- 19. The vector of claim 18, wherein said *Salmonella typhi* vector is CVD908-htrA or CVD908.
- 5 20. The vector of claim 16, wherein the attenuated Salmonella vector is a Salmonella typhimurium vector.
 - 21. The vector of claim 20, wherein said *Salmonella typhimurium* vector is BRD509 or BRD807.
 - 22. The vector of claim 16, wherein said attenuated Salmonella vector further comprises an htrA promoter.

10

23. The vector of claim 16, wherein said attenuated Salmonella vector further comprises a *nirB* promoter.

PCT/US00/30191

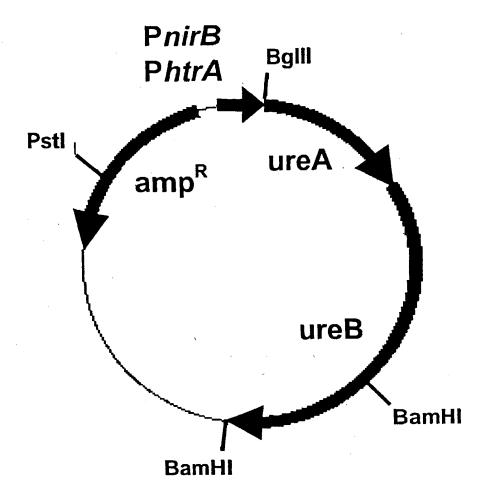


Fig. 1

Figure 2. Mucosal priming with S. typhimurium vectored urease followed by parenteral boosting with alum induces an IgG2a humural immune response equivalent to that induced by mucosal priming with LT.

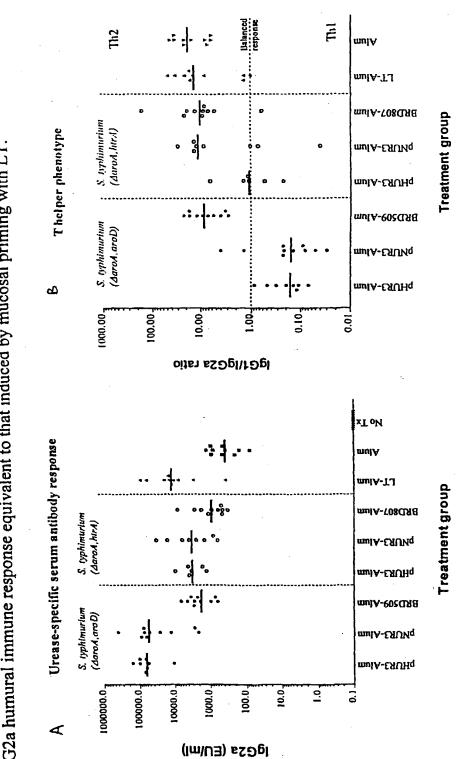


Figure 3. Mucosal priming with attenuated S. typhimurium::ure A/B affords equivalent protection as LT in a prime-boost regimen with Alum

		P-value	0.0002	0.003	ı		0.004	900'0	•	<0.0001	0.01		
	æ	Group A log10 CFU S. typhimurium darod, aro D	1. pHUR3-Alum 1.69	2. pNUR3-Alum 1.45		S. typhimurium darod, htr d		pNUR3-Alum	6. BRD807-Alum 0.37	7. LT-Alum 2.15			
					··i	! •	•					×T oH	and, and innedB and, and and, histinadB and, hist
		Protective eMency with S Ophimurium vectored urense		•	•				•			maiA	
		cctored						•	<u></u>		•••••	coulA-TJ	
		erium v	F - F		• 3	• • •	•					mulA-YOSCIAE	ii ii
臣		Ophlm	S. syphimurium (Amrud, Mrd)			••	4	••	• •			mulA-ETUMq	Treatment
I All		rith S					<u> </u>					mulA-UNUHq	•
WIE		Певсу	1a			•• þ	.1					contA-902CIAE	
men		ctive el	S. typkimurium (durnd,umi))			•	·· ·	١.	• :-			mulA-ENDMq	-
regii		Prote	NZ		•		• •	• }		•		mulA-UNUHq	
ime-boost regimen with Alum			10000000	100000		10000	0,000		8			788	
ime-l	∢				elturi ()	i pyłori (Kagoid)	tive H FUm	#1i1 (C)	Quan				

Page 1

Fig. 4 (10f4)

	ACACAGCAATTTAGATATTAATCATCCACAGGAGAGATCTCCATGAA	90
	- Ure =	
PhtrA	TOOFRY, SSTGEISMK	
	GGAGAATTGGCTAAAAAACGCAAAGAAAAAGGCATTAAGCTTAACTA	
	<u> </u>	180
	UreA ————————————————————————————————————	
	G E L A K K R K E K G I K L N Y GCGAGAGCTGGTAAAAAGACTGCGGCTGAATTGATGCAAGAAGGGCG	
GTAGAAGCAGTAGCTTTGATTAGTGCCCATATTATGGAAGAAG	BLEAGAGE 166 TANANAGAE 16C66C 15AAT 15AT 6CAAGAAGGGCG	270
	UreA	
	A R A G K K T A A E L M O E G R	
ACTOTTTAAAACCAGATGATGTGATGGATGGCGTGGLAAGLA	ATGATCCATGAAGTGGGTATTGAAGCGATGTTTCCTGATGGGACTAA	360
	UreA ————————————————————————————————————	
	HIHEVGIE AHFPDGTK	
CTCGTAACCGTGCATACCCCTATTGAGGCCAATGGTAAATTAG	STTCCTGGTGAGTTGTTCTTAAAAAATGAAGACATCACTATCAACGA	450
	JreA	
LYTYHTPIEANGKL	V P G E L F L K N E D I T I N E	
GGCAAAAAGCCGTTAGCGTGAAAGTTAAAAATGTTGGCGACA	AGACCGGTTCAAATCGGCTCACACTTCCATTTCTTTGAAGTGAATAG	540
V	JreA ====================================	•
G K K A V S V K V K N V G D	$ \begin{picture}(cccccccccccccccccccccccccccccccccccc$	
TGCCTAGACTTTGACAGAGAAAAACTTTEGGTAAACGCTTAG	GACATTGCGAGCGGGACAGCGGTAAGATTTGAGCCTGGCGAAGAAAA	630
U Company	JreA -	
CLDFDREKTFGKRL	D I A S G T A V R F E P G E E K	
TCCGTAGAATTGATTGACATTGGCGGTAACAGAAGAATCTTTG	GGATTTAACGCATTGGTTGATAGACAAGCAGACAACGAAAGCAAAAA	720
	UreA	720
	G F N A L V D R O A D N E S K K	
ATTECTTTACACAGAGCTAAAGAGCGTGGTTTTCATGGCGCTA	AAAAGCGATGACAACTATGTAAAAAACAATTAAGGAGTAAGAAATGAA	810
lina =	■ Ure ■	810
	K S D D N Y V K T I K E . E H K	
AAAGATTAGCAGAAAAGAATATGTTTCTATGTATGGTCCTACTA	ACAGGCGATAAAGTGAGATTGGGCGATACAGACTTGATCGCTGAAGT	000
 		900
	UreB T G D K V R L G D T D L I A E V	
	GGCGGTAAAACCCTAAGAGAAGGCATGAGCCAATCTAACAACCCTAG	
KISRKEYVSMYGPT		990
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG		
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG	UreB	
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG U	UreB G K T L R E G M S O S N N P S	
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA	
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAGAGTTGGATTTAATCGTGG	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UreB	1080
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAGGTTGGATTTAATTATCACTAACGCTTTAATCGTGG	UTEB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UTEB D Y T G I Y K A D I G I K D G K	1080
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAGGTTGGATTTAATTATCACTAACGCTTTAATCGTGG	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UreB	1080
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAGGTTGGATTTAATTATCACTAACGCTTTAATCGTGG K E E L D L I I T N A L I V AATCGCTGGCATTGGTAAAGGCGGTAACAAAGACATGCAAGATG	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UreB O Y T G I Y K A D I G I K D G K GGCGTTAAAAACAATCTTAGCGTAGGTCCTGCTACTGAAGCCTTAGC	1080
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAAGATTGATTAATTATCACTAACGCTTTAATCGTGG K E E L D L I I T N A L I V AATCGCTGGCATTGGTAAAGGCGGTAACAAAGACATGCAAGATG	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UreB O Y T G I Y K A D I G I K D G K GGCGTTAAAAACAATCTTAGCGTAGGTCCTGCTACTGAAGCCTTAGC UreB G V K N N L S V G P A T E A L A	1080
K I S R K E Y V S M Y G P T AGAACATGACTACACCATTTATGGCGAAGAGCTTAAATTCGGTG E H D Y T I Y G E E L K F G CAAAGAAGAAGATTGATTAATTATCACTAACGCTTTAATCGTGG K E E L D L I I T N A L I V AATCGCTGGCATTGGTAAAGGCGGTAACAAAGACATGCAAGATG	UreB G G K T L R E G M S O S N N P S GATTACACCGGTATTTATAAAGCGGATATTGGTATTAAAGATGGCAA UreB D Y T G I Y K A D I G I K D G K GGCGTTAAAAACAATCTTAGCGTAGGTCCTGCTACTGAAGCCTTAGC UreB G V K N N L S V G P A T E A L A ATCCACTTCATTTCACCCCAACAAATCCCTACAGCCTTTTGCAAGCGG	1080

Fig. 4 (20f制

	•		AIG		GIO	GTG	GAA	ACC	GGT	CCT	GCT	GAT	GGL	ALIA	ATGE	ACI	AC 17	LILA	. 10	CAG	GCA	GAAL	AA	4///		4166	<u></u> 1
			_						_			_	_	UreB		_			_	_	_				_	_	_
v	т	т	M	1	G	G	G	T	G	Р	Α	D	G	T	N A	T	T	1	T	P	G	R F	₹ 1	N L	K	W	M
															AAGGT												
.11	AGA	666	661	UAA!						110																	- 1
														IIreR						_							_
	_			_	_										K G										n	1	F
_																											
CC	GGT	GCG	ATT	GGC.	1110	CAA	ITTC	CAC	GAA	GAC	TGG				רזזכז			ATC	ATG	CGT	TAG	ATGT	TGC	GGA	CAA	HAC	GA 1!
																											- 1:
_	_	_	_	_	•		_												_		_	-					_
Α	G	Α	1	G	F	A	ı	н	Ε	D	W	G	T	Ŧ	P 5	A.	i	N I	H	A !	L	D V	,	A D	K	Y	D
:16	. r a a	cT.	GCT	ATC	sec.	ACAC	SAC/	ACT	TTG	AAT	GAAG	SCC	GGT	TGTG	TAGAA	GAC	ACTA	TGG	CTG	CTA	TTG	CTGG	ACE	CAC	TATO	CAC	AÇ
	-							_																			10
				_					_				_	UreB													
v		v	_			т									V E							A G	: F	₹ Т	н	н	T
															AAGTA												
TC	CAC	ACT.	GAA	GGCI	3C 1 (36CG	الماة	اهناند	LALI	9C 11		3A I	A 1 1	AIIA	AAGIA	IGEL	6616	MAL.	4CA	ALA			LGL		LAL	MAC	<u> </u>
														las D													`
-	_		_	_																							_
															K V												
CC	ATC	CCT	TTC	ACC	STG	ATA	1CAC	GAAG	GCA	GAG	CACA	ATG(GAC	ATGC	TTATG	GTG	TGCC	ACCA	\CT	TGG	ATA	AAAG	CAT	TAA	AGAA	GAT	GT
																		4								,	- → 18
_	_	_	_	_		_	-																				
T	ŧ	Р	F	T	٧	N	T	Ε	A	Ε	Н	H	D	H	LH	٧	C	H F	1	L	D 1	K 5	1	K	Ε	D	٧
					_	am F																					
					-1																						
AG	TTC	GC1	GAT	TCA	4GG	ATC	cecr	CCTI	CAA	ACC.	ATTO	CG	GCTI	GAAG	ACACT	TTG	CATG	ACAT	IGG	GGA,	TTT.	TCTC	AAT	CAC	CAGT	TCT	GA
																											<u> 18</u>
_			_				اسيد			_		_		UreB			_	_				_				_	-
n	F	Δ	ถ	s	R	1	R	P	۵	T	1	A	A	Ε	D T	L	н	D t	1	G	1 1	F 5		T	5	S	D
															AAACA												
	LAA	1011	- A 1 G																-								18
,_														UreB						_			_			_	_
	_			_		ν	c	F	v						G T										Ł	κ	Ε
AA	AAA/	GGG	GAT	AAC	GAC.	AAC`	116/	AGG/	A I C	AAA					AATAC					LOA		LICA	100				<u></u> 20
														land.													_
					_	_	_	_																			
				м			_	•								-									•		v
TA	AGGI																	N F									
_		TIC	AGTA												K Y GTCCA		TTCT	TTG	CG	TGA	AACI	CCAA	CAT				ee
_		TTC	AGTA	GAA	GTG	GC	AAA	GTG	GCT	GAC	TTGC	ATE:	TTG	TGGA	GTCCA	GCA	TTC1	TTG	CG	TGA	AACI	CCAA	CAT				
	_		_	GAA	GTG	GC	AAA	GTG	GCT	GAC	TTG	ATE	TTG	TGGA UreB	GTCCA	GCA	TTCT	TTG	CG	TGA	AAC	CCAA	CAT	GAT	CATO	AAA	GG 21
٧	6		_	GAA	GTG	GC	AAA	GTG	GCT	GAC	TTG	ATE	TTG	TGGA UreB	GTCCA	GCA	TTCT	TTG	CG	TGA	AAC	CCAA	CAT	GAT	CATO	AAA	GG 21
۷	G	s	v	GAA E	ete V	e Gec	AAA(GTG(GC T	GAC D	TTG(ATE V	TTG	TGGA UreB W	GTCCA S P	AGCA	TTC1	TTG(GC G	TGA,	AACI K	P N	CAT	GAT	CATO	K	G 21 G
V G	G ATT	s	v	GAA E	ete V	e Gec	AAA(GTG(GC T	GAC D	TTG(ATE V	TTG	TGGA UreB W	S P	A CCA	F CAAC	TTG(GCG G	TGA: V	AACI K	P N	CAT	GAT	CATO	K	G 21 G
V G	G ATT	s	v	GAA E	ete V	e Gec	AAA(V GGC	A GAT	GAC D GCG	L AAC	V GCT	L TCT	UreB W	S P	A CCA	F CAAC	F (GCG G	TGA: V	AACI K	P N	CAT	GAT	CATO	K	GG 21 - G CA
G/	ATT	S	V TGC0	E TTA	V AGC	G G CAA	K ATG	V GGC	A GAT	D GCG	L AAC	V GCT	L TCT	UreB W ATCC UreB	S P	A CCCA	F CAAC	F (ccc)	GCG	TGA: V ATT:	AACI K ACAI	P N	CAT	GAT	CATO	K	GG 21 G CA 22
G/	ATT(S	V TGCC	E TTA	V AGC	G G CAA	K ATGI	V GGC	A GAT	D GCG	L AAC(V GCT	L TCT.	TGGA UreB W ATCC UreB	S P CTACC	A CCCA P	F CAAC	F (ccc)	GCG FTT	V ATT	AACI ACAI Y	P N GAGA	CAT	GAT	I CGC	K CAT	GG 21 G CA 22
G/	ATT(S	V TGCC	E TTA	V AGC	G G CAA	K ATGI	V GGC	A GAT	D GCG	L AAC(V GCT	L TCT.	TGGA UreB W ATCC UreB	S P	A CCCA P	F CAAC	F (ccc)	GCG FTT	V ATT	AACI ACAI Y	P N GAGA	CAT	GAT	I CGC	K CAT	GG 21 G CA 22
G/	ATT(S	V TGCC	E TTA	V AGC	G G CAA	K ATGI	V GGC	A GAT	D GCG	L AACO N GTG	V GCT A	L TCT. S CAA	UreB W ATCC UreB	S P CTACO	A CCCA P	F CAAC	F (ccc)	GCG FTT	V ATT	AACI ACAI Y	P N GAGA	CAT	GAT	I CGC	K CAT	GG 21 G CA 22 H CA
G G G	F TAA	S CAT I AGC	Y TGCC A TAA	E STTA	V AGC S GAT	G G CAA O GCA	K ATGI H AAC	V GGC G	A GAT D	D GCG A	L AACO N GTG	V GCT A	L TCT S CAA	UreB W ATCC UreB I GCGG	S P CTACO P T	A CCCA P	F CAAC O	F (CGGT	GCG FTT V	Y ATT	AACI ACAI Y I	P N GAGA R E	AAT	GAT	CGCT	K CAT H	GG 21 G CA 22 H CA 23
G G G	F TAA.	S CAT I AGC	V TGCC	E STTA L	V AGC S GAT	GGCA CAAA O GCA	K ATGI H AAC	V GGC G	A GAT	D GCG	L AACO N GTG	V SCT	L TCT. S CAA	UreB W ATCC UreB GCGG UreB	S P CTACC	A CCCA	F CAAC	F CCGGT	GCG G FTTT V TTA	Y AAG	AACACACACACACACACACACACACACACACACACACA	P N GAGA R E AATT	CAT	GAT	I CGC1	K CAT H AAGA	GG 21 G CA 22 H CA 23
G G G	F TAA.	S CAT I AGC	V TGCC	E STTA L	V AGC S GAT	GGCA CAAA O GCA	K ATGI H AAC	V GGC G	A GAT	D GCG	L AACO N GTG	V SCT	L TCT. S CAA	UreB W ATCC UreB GCGG UreB	S P CTACC	A CCCA	F CAAC	F CCGGT	GCG G FTTT V TTA	Y AAG	AACACACACACACACACACACACACACACACACACACA	P N GAGA R E AATT	CAT	GAT	I CGC1	K CAT H AAGA	GG 21 G CA 22 H CA 23 AC
G G G	F TAA.	S CAT I AGC	V TGCC	E STTA L	V AGC S GAT	GGCA CAAA O GCA	K ATGI H AAC	V GGC G	A GAT	D GCG	L AACO N GTG	V SCT	L TCT. S CAA	UreB W ATCC UreB GCGG UreB	S P CTACO P T	A CCCA	F CAAC	F (CGGT	GCG G FTTT V TTA	Y AAG	AACACACACACACACACACACACACACACACACACACA	P N GAGA R E AATT	CAT	GAT	I CGC1	K CAT H AAGA	GG 21 G CA 22 H CA 23
G G G	F TAA.	S CAT I AGC	V TGCC	E STTA L	V AGC S GAT	GGCA CAAA O GCA	K ATGI H AAC	V GGC G	A GAT	D GCG	L AACC N GTG	V GCT	L TCT S CAAA	UreB W ATCC UreB GCGG UreB A	S P CTACC P T CTTAT	A CCCA	F CAAC O AAAC K	F (CGGT	GCG G FTTT V TTA	Y AAG	AACACACACACACACACACACACACACACACACACACA	P N GAGA R E AATT	CAT	GAT	I CGC1	K CAT H AAGA	GG 21 G CA 22 H CA 23 AC
G G G	F TAA. K	S CAT	V TGCC A TAAA K	E STTA L ATAC	V AGC S GAT D	G G CAAA O GCA A TGC	K ATGI H AAC	y GGC G ATC	A GAT	D GCG A TITT	L AACC N GTG	V GCT	L TCT S CAA	TGGA UreB W ATCC UreB I GCGG UreB A ATGC	S P CTACC	A CCCA P GAAC	F CAAC	F (CCGGT)	GCG G ITT V I I CCG	Y AAG	AACA ACA AAAG	P N SGAGA	CAT LAAT AGG	GATI	I CGCT	K CAT H AAGA R	G
G G G G G G G G G G G G G G G G G G G	F TAA	S CAT	V TGCC A TAAA K	E STTALL LATAC	V AGC	G CAAA	K ATGI H AAC	GTGG GGGC GATC	A GAT	B GCG A TIT	L AACC N GTG V AAAA	V GCT	L TCT S CAA O GAC	TGGA UreB W ATCC UreB GCGG UreB A ATGC UreB H	S P CTACC P T CITAT	A CCCA P TGAC D CAAC	F CAAC	F (CCGGT	GCG G ITT I CCG	V ATT. Y AAG. K CTC.	AACA AACA Y AAG AACA H	P N GAGAATT	CATI LAAT AGG	GATTING I I I I I I I I I I I I I I I I I I	I CCGCT	K CAT H AAGA R IGAA	GG 21 G CA 22 H CA 23 AC 24
G G G G G G G G G G G G G G G G G G G	F TAA	S CAT	V TGCC A TAAA K	E STTALL LATAC	V AGC	G CAAA	K ATGI H AAC	GTGG GGGC GATC	A GAT	B GCG A TIT	L AACC N GTG V AAAA	V GCT	L TCT. S CAA O GAC	TGGA UreB W ATCC UreB I GCGG UreB A ATGC UreB H GCCA	S P CTACO P T CTTAT A Y AATTO	A CCCA P TGAC D CAAC	F CAAC	F (CCGGT	GCG G ITT I CCG	V ATT. Y AAG. K CTC.	AACA AACA Y AAG AACA H	P N GAGAATT	CATI LAAT AGG	GATTING I I I I I I I I I I I I I I I I I I	I CCGCT	K CAT H AAGA F GAA	GG 21 G CA 22 H CA 2: AC 2: TT
G G G G ST	F TAA	S CAT	V TGCC A TAAA K	E STTALL LATAC	V AGC	G CAAA	K ATGI H AAC	GTGG GGGC GATC	A GAT	B B B B B B B B B B B B B B B B B B B	L AACC N GTG V AAAA	V GCT	L TCT S CAAA O GAC	TGGA UreB W ATCC UreB I GCGG UreB A ATGC UreB H GCCA	S P CTACC	A CCCA P IGAC D NAGTG	F CAAC	F (CCGGT	GCG G ITT I CCG	V ATT. Y AAG. K CTC.	AACA AACA Y AAG AACA H	P N GAGAATT	CATI LAAT AGG	GATTING I I I I I I I I I I I I I I I I I I	I CCGCT	K CAT H AAGA F GAA	GG 21 G CA 22 H CA 23 AC 24
G G G G T A	F TAA K GTT	S CAT I AGC AGC FTGT	V TGCC	E STTA	V AGC S GAT D AAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AACL N AGA	GTGG V GGCC G AATC	A GAT	B B B B B B B B B B B B B B B B B B B	L AACO	V GCT	L TCT. S CAAA O GAC	TGGA UreB W ATCC UreB GCGG UreB A TGC UreB A TGC H GCCA	S P CTACCO	A CCCA P IGAC D CAAC	F CAACO O AAAAG K GGACA	F (CCGGT	G CG	Y AATT. Y AAAG	AACAI Y AAGAI AACAI H TCT	P N SAGA	AAAT	GATI	A TGAA	K CAT H AAGA R GGAA	GG 21 G CA 22 G CA 21
G G G G T A	F TAA K GTT	S CAT I AGC AGC FTGT	V TGCC	E STTA	V AGC S GAT D AAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AACL N AGA	GTGG V GGCC G AATC	A GAT	B B B B B B B B B B B B B B B B B B B	L AACO	V GCT	L TCT. S CAAA O GAC	TGGA UreB W ATCC UreB GCGG UreB A TGC UreB A TGC H GCCA	S P CTACC	A CCCA P IGAC D CAAC	F CAACO O AAAAG K GGACA	F (CCGGT	G CG	Y AATT. Y AAAG	AACAI Y AAGAI AACAI H TCT	P N SAGA	AAAT	GATI	A TGAA	K CAT H AAGA R GGAA	GG 21 G CA 22 G CA 21
G G G ST	F TAA K GTT	S CAT I AGC AGC FTGT	V TGCC	E STTA	V AGC S GAT D AAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AACL N AGA	GTGG V GGCC G AATC	A GAT	B B B B B B B B B B B B B B B B B B B	L AACC	V GCT A TCT S AAAA K AAAA	L TCT. S CAAA O GAC	TGGA UreB V ATCC UreB GCGG UreB A ATGC UreB A ATGC	S P CTACCO	A CCCA P IGAC D CAAC	F CAACO O AAAAG K GGACA	F (CCGGT	G CG	Y AATT. Y AAAG	AACAI Y AAGAI AACAI H TCT	P N SAGA	AAAT	GATI	A TGAA	K CAT H AAGA R GGAA	GG 21 G CA 22 G CA 21
G G G T A	F TAA. K GTT	S CAT	V TGCC	E STTALL LATAC	V AGC S GAT D AAAT N GGAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AACC N AGA	G G G G ATC	A GAT	D GCG A TITT F ACT	L AACC N GTG V AAAA K TCT	V GCT A TCT S AAAA K AAAA	L TCT. S CAA O GAC O Ure P n HI	TGGA UreB W ATCC UreB GCGG UreB A ATGC H GCCA	S P CTACC P T CTTAT A Y AATTI	A CCCA PIGAC D CAAC	F CAACO O AAAAG K K GACO O B AAAAG S S S	F (CCGGT	GCG TTTA TCGC	Y AAAG	AACAI Y AAAG	P N SGAGAATT	CAT	GATI	I CGCT	K CAT H AAGA R FGAA E GGAT	GG 21 G CA 22 H CA 22 G AC 24 TT 25 F
G G G T A	F TAA. K GTT	S CAT	V TGCC	E STTALL LATAC	V AGC S GAT D AAAT N GGAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AACC N AGA	G G G G ATC	A GAT	D GCG A TITT F ACT	L AACC N GTG V AAAA K TCT	V GCT A TCT S AAAA K AAAA	L TCT. S CAA O GAC O Ure P n HI	TGGA UreB W ATCC UreB GCGG UreB A ATGC H GCCA	S P CTACC P T CTTAT A Y AATTI	A CCCA PIGAC D CAAC	F CAACO O AAAAG K K GACO O B AAAAG S S S	F (CCGGT	GCG TTTA TCGC	Y AAAG	AACAI Y AAAG	P N SGAGAATT	CAT	GATI	I CGCT	K CAT H AAGA R GGAAT O D	GG 21 G CA 22 H CA 23 G AC 24 T T T 25 F F GGT
G G G T Y	F TAA. K GTT L CCA	S CAT	V TGCC	E STTA	V AGC S GAT D AAAT N GGAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AAC N AGA K	GTGG V GGGCG G ATC I AATT N AGAA	A GAT	B G G G G G G G G G G G G G G G G G G G	L AACCO N GTG	STA V GCT A TCT S AAAA K AAAA GAT	L TCT. S CAAA O GAC O CCAA O CCAA O CCAA O CCCA O C	TGGA UreB GCGG UreB ATGC UreB GCCA	S P CTACCETAL A Y AATTO	A CCCAACO N AGTG	F CAACOO O O O O O O O O O O O O O O O O	F (CCGGT) P (CCGGT) GGCA T (CTA)	GCG GTTT VTTA CCGC	V I ATT. Y AAG K CTC. A AAC	AACAI Y AAGA AACA H TCT	P N GAGAGARR E L LTTGA	CAT HAAT AGE	GATION IN THE STATE OF THE STAT	A TGAA	K CAT HAAGA R GGAA E GGAT D	GG 21 G CA 22
	F TAA. K GTT L CCA	S CAT	V TGCC	E STTA	V AGC S GAT D AAAT N GGAT	GGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	K ATGI H AAC N AGA K	GTGG V GGGCG G ATC I AATT N AGAA	A GAT	B G G G G G G G G G G G G G G G G G G G	L AACCO N GTG	STA V GCT A TCT S AAAA K AAAA GAT	L TCT. S CAAA O GAC O CCAA O CCAA O CCAA O CCCA O C	TGGA UreB GCGG UreB ATGC UreB GCCA	S P CTACC P T CTTAT A Y AATTI	A CCCAACO N AGTG	F CAACOO O O O O O O O O O O O O O O O O	F (CCGGT) P (CCGGT) GGCA T (CTA)	GCG GTTT VTTA CCGC	V I ATT. Y AAG K CTC. A AAC	AACAI Y AAGA AACA H TCT	P N GAGAGARR E L LTTGA	CAT HAAT AGE	GATION IN THE STATE OF THE STAT	A TGAA	K CAT HAAGA R GGAA E GGAT D	GG 21 G CA 22

Fig. 4 (3 of 4).

CCTGGCCACGGGTGCGCATGATCGTGCTCCTGTCGTTGAGGACCCGGCTAGGCTGGCGGGGTTGCCTTACTGGTTAGCAGAATGAAT	
	2700
LATGAHDRAPVYEDPARLAGLPYWLAE IT	
and the second s	2 790
D T R A N V K R L L L O N V C D L S N N M N G L R F P C F V AAAGTCTGGAAAGGCGGAAGTCAGCGCTCTTCCGCTTCCGCTCGCT	
	2880
K S G N A E V S A L P L P R S L T R C A R S F G C G E R Y O	
GCTCACTCAAAGGCCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAAAGGCCAGCAAAAAGGCCAGG	2970
Origin	
L T O R R . Y G Y P O N O G I T O E R T C E O K A 5 K R P G AACCGTAAAAAGGCCGCGTTGCTGGCGTTTTTCCATAGGCTCGCCCCCCTGACGAGCATCACAAAAATCGACGCTCAAGTCAGAGGTGG	
AACEGTAAAAAGGELGEGTTELTGGGGGTTTTTCCATAGGETCCGCCCCCTGACGAAAAATCCGCCCCCAAAAAATCCGCCCCCCAAAAAAACGCACGC	3060
Origin THE DROCK PESICS APLISITED A DVRGG	
T V K R P R C W R F S I G S A P L T S I T K I D A O V R G G CGAAACCCGACAGGACTATAAAGATACCAGGCGTTTCCCCCTGGAAGCTCCCTCGTGCGCTTTCCGGCCCTTACCGGA	
	3150
Origin FTRODYKOTRRFPLEAPSCALLFRPCRLPD	
TACCTETICTCCTTTCTCCCTTCGGGAAGCGTGGCGCTTTCTCAATGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCGTTCGCTCC	
	3240
Origin T C P P F S L R E A W R F L N A H A V G I S V R C R S F A P	
AAGT TEGET TETTTETATGAACCCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCCGGTAAGACAC	3330
Origin	
SWAVCINPPFSPIAAPYPVIIVLSPIR.DI	
GACTTATCGCCACTGGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAGTTCTTGAAGTGGTGGCCT	3420
Origin	
TYRHWOOPLVIGLAERGM.AVLOSS.SGGL	
AACTACGGCTACACTAGAAGGACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTTACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCC	3510
Origin S.O.L.P.S.F.K.F.L.V.A.L.D.P.	
T T A T L' E G O Y L V S A L C . S O L P S E K E L V A L D P GGCAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTTGCAAGCAGCTAGCAGATTACGCGCAGAAAAAAAGGATCTCAAGAAGATCCTTTG	
GELAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTTTTTTT	3600
Origin ANKPPL VAV V F L F ASSRLRAEKK D L K K I L .	
ATCITITICACCCCTTCTCACCCTCAGTGGAACGAAAACTCACGTTAAGGGATTTTGGTCATGAGATTATCAAAAAGGATCTTCACCTAG	
	3690
ATCCTTTTAAATTAAAAATGAACTTTTAAATCAATCTAAAGTATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAG	
Amor	3780
SF. J K N E V L N O S K V Y M S K L G L T V T N A . S V R	
ACCOUNT OF THE CONTROL OF THE CONTRO	2070
AmpR	3670
HISORSVYFVHP, LPDSPSCR, LRYGRAYH	
TOTAL CONTROL OF THE TATAL CONTRACTOR AND AND CONTRACTOR AND CONTR	3960
AmpR	2000
LAPVLO, YRETHAHRLOIYOO, T50 PEGP5	
	4050
	–
A E V V L O L Y P P P S S L I V A G K L E . V V R O L I V	

Fig. 4 (4 of 4)

Pst i

	_	_	_				_					-				•												_		
1	_	_	•••	•	-	•		•		_			_							-		_	L	_	•	_	_			-
												LIL											TGT	LUA		GAI	CAI	311/	GAL	IGGI
																										_		_	_	-
	•	-	•		-	•	-	-	_	-	-	_					_					_	C		•	_	•-	-	-	G
4:	CC	CAA	CT	AGT	GTG	CTG	IGA	ETG	111	3CT	GAT	IAA		CAI	IIGC	ILLA	IC 1G		CIC	ATI	ATA	TGC	CAC	CAG	TGG	TTA	TGG	TC	CAC	TAT
	-				-						_	_			R	Amp	-		-									_		
	•	-	-	_		_	-	_									_			-	-	_	Н	-		_		_		
4		CTT	AA	GCAG	ATA	CAC	CGC	CCG	ATA	ATA	GGG	CAC	CAA	CGI	CGG	GCU	CII	GC I	GII	.CGA	GAC	GGC	TGC	GTA	AGT	TAA	GAG	TC	CA	AG
	_											-				•								-						
	-	_	_		-			-	-	-	_		_								_	_	C	-	_		_	_		_
45			-																				GTT	1			TCA	TC	TGC	AAC
	_		٠.						_		_	_			R=	4mp	_	_	_	_				_		_		_		
																							٧							
45	I A	AAT	GGG	AAA	CAA	CGG	ITG	IAAA	3GC/	AA(AGE	AAAI	CAA	GAG	GGI	CIG		GCG	CCA	TCA		TTA	CTT	CAT	CAG	CTT	GAT	ACT	CC/	CAC
	-					_		-	_			-	-		R=	\m p		-		-	-				_	_		-	_	-
		_		-							_		_	_							-	_	L		_	_	_			
46																							TAC				GGA	CAC	CGA	GGG
																					•									_
	-	_		•	-		-			-			_						-	-		-	. Y	_			_			G
	11	IAI	CAI	AAC	AGA	C 17	CGI	TGA	ACC	GCC	AG	GAAA	CCC		CAI	GLA	CGC		366	TAG	AAA	AAC	ATA	AAA	AGA	111	GTA	AAI	116	TAI
47										_		Ε	_	_			_	_	_				_		٠ ـــ	_				

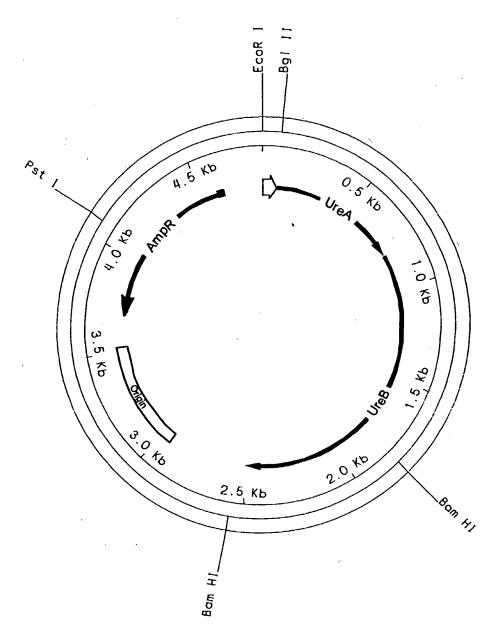


Fig. 5

SEQUENCE LISTING

```
<110> OraVax, Inc.
<120> Use of salmonella vectors for
 vaccination against helicobacter infection
<130> 06132/060WO1
<150> US 09/431,705
<151> 1999-11-01
<160> 52
<170> FastSEQ for Windows Version 4.0
<210> 1
<211> 4824
<212> DNA
<213> Artificial Sequence
<220>
<223> includes sequences from Helicobacter pylori,
      Salmonella typhimurium, and Escherichia coli
<221> CDS
<222> (2)...(31)
<221> CDS
<222> (41)...(61)
<221> CDS
<222> (65)...(799)
<221> CDS
<222> (803)...(2512)
<221> CDS
<222> (2516)...(2692)
<221> CDS
<222> (2696)...(2896)
<221> CDS
<222> (2900)...(3322)
```

<221> CDS

<222> (3326)...(3385)

```
<221> CDS
<222> (3389)...(3406)
<221> CDS
<222> (3410)...(3466)
<221> CDS
<222> (3470) ... (3598)
<221> CDS
<222> (3602)...(3661)
<221> CDS
<222> (3665)...(3697)
<221> CDS
<222> (3701)...(3769)
<221> CDS
<222> (3773)...(3817)
<221> CDS
<222> (3821)...(3844)
<221> CDS
<222> (3848)...(3889)
<400> 1
g aat tot att ccg gaa ott cgc gtt ata aaa tgaatotga cgt aca cag
                                           Arg Thr Gln
 Asn Ser Ile Pro Glu Leu Arg Val Ile Lys
caa ttt aga tat taa tca tcc aca gga gag atc tcc atg aaa ctc acc
                                                                  97
Gln Phe Arg Tyr Ser Ser Thr Gly Glu Ile Ser Met Lys Leu Thr
    15
cca aaa gag tta gat aag ttg atg ctc cac tac gct gga gaa ttg gct
                                                                  145
Pro Lys Glu Leu Asp Lys Leu Met Leu His Tyr Ala Gly Glu Leu Ala
     30
aaa aaa cgc aaa gaa aaa ggc att aag ctt aac tat gta gaa gca gta
                                                                  193
Lys Lys Arg Lys Glu Lys Gly Ile Lys Leu Asn Tyr Val Glu Ala Val
                     50
45
get ttg att agt gee eat att atg gaa geg aga get ggt aaa aag
Ala Leu Ile Ser Ala His Ile Met Glu Glu Ala Arg Ala Gly Lys Lys
                 65
act gcg gct gaa ttg atg caa gaa ggg cgc act ctt tta aaa cca gat
Thr Ala Ala Glu Leu Met Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp
             80
                                 85
```

gat gtg a			Ala S	-			_				_	337
gcg atg t Ala Met I 110					_							385
gag gcc a Glù Ala A 125			_			_					_	433
gac atc a Asp Ile T		-			_		-			_		481
aat gtt o	-		•		Gly							529
gaa gtg a Glu Val A		_	Asp P		_	_						577
cgc tta c Arg Leu A 190												625
gaa aaa t Glu Lys S 205	_	-	-	_				_	_			673
gga ttt a	-		_	_	_	_			_			721
att gct t Ile Ala J			_		Gly						-	769
gat gac a Asp Asp A		_	Thr I				_	Met 1		aag Lys 1		817
agc aga a Ser Arg :	_	_	Ser M	•						_		865
gtg aga f Val Arg l		-	_	_	-	_	_					913

1537

	285					290					295					
				_							ggt Gly				_	961
		_	_	_					-		gaa Glu		_	_		1009
				_			- , -	_			ggt Gly					1057
~									_		att Ile					1105
		-			-						ctt Leu 375		-			1153
_			~				_		_	_	gta Val	_				1201
	_		_								caa Gln					1249
	_	_		_			_				gga Gly				_	1297
				_							aga Arg					1345
					Ala					Met	aat Asn 455					1393
											gcc Ala					1441
_		_				~			-	-	tgg Trn					1489

Ala Gly Ala Ile Gly Phe Ala Ile His Glu Asp Trp Gly Thr Thr Pro

tct gca atc aat cat gcg tta gat gtt gcg gac aaa tac gat gtg caa

Ser	Ala	Ile	Asn 495	His	Ala	Leu	Asp	Val 500	Ala	Asp	Lys	Tyr	Asp 505	Val	Gln	
_	_	_	_	_	gac Asp											1585
	_	_	_		gct Ala				_						-	1633
	_				cac His 545	-		_					-		_	1681
					gct Ala											1729
		_			cac His	_	_	_		_		_			_	1777
		~			gaa Glu	_	_	_			_				_	1825
					gct Ala	_			_		-			_		1873
	_		_		gac Asp 625		_		_		-				-	1921
		_			caa Gln		-	_			_		_			1969
			_	_	aaa Lys		-		_							2017
	-				acc Thr											2065
					gta Val									44		2113

	_		_							aac Asn 710	_					2161
					_		_		_	gcg Ala						2209
			-	_				_	_	ttc Phe	_					2257
_			-	_						tct Ser			~		_	2305
					_					aga Arg	_		-	_	-	2353
			~						_	atg Met 790				_		2401
	_			_	_			_		tac Tyr					-	2449
			_					_		aaa Lys		-	_			2497
	ttt Phe	. –	_	_	_	_	Phe 1			gca Ala :		Leu I		-		2545
_	Gly			_	_					atg Met	_					2593
		_	_		_	-	-	_		gcg Ala		_		_		2641
	Val									ttg Leu 885						2689
gaa Glu				Asp	_	_			Val :	aag Lys 1 900	_	_	_	Leu (2737

	gtc Val		_	_				_						_	_	2785
	gta Val						_	_				_				2833
	ctg Leu		-	_						_		_			-	2881
	act Thr 955	_				tyr (-	Asn (_	2929
_	gaa Glu 970	_		_			_		_					_	_	2977
	agg Arg	_	- ,	_		Arg					Ser	_		_	_	3025
_	atc Ile				Asp	_		_		Gly		_		_	Gln	3073
_	tat Tyr		_	Thr		_			Leu	_	-		_	Cys	-	3121
	ctg Leu		Arg		_	_		Pro	_		_	-	Pro	_		3169
	cgg Arg 1050	Glu					Leu					Va1				3217
_	cgg Arg	_		_		Ala		_			Val		-			3265
	ttc Phe				Ala					Val					Ser	3313
	acc Thr			_		act Thr		_			_	_		-	_	3361

1100	1105 1110	
aca gga tta gca gag cga ggt Thr Gly Leu Ala Glu Arg Gly 1 1115	atg tag gcg gtg cta cag agt tct Met Ala Val Leu Gln Ser Ser 1120 1125	3406
	gct aca cta gaa gga cag tat ttg gta Ala Thr Leu Glu Gly Gln Tyr Leu Val 1135	
	tta oct tog gaa aaa gag ttg gta got eu Pro Ser Glu Lys Glu Leu Val Ala 1150 1155	
,	ccg ctg gta gcg gtg gtt ttt ttg ttt Pro Leu Val Ala Val Val Phe Leu Phe 1165 1170	
	gaa aaa aag gat ctc aag aag atc ctt Glu Lys Lys Asp Leu Lys Lys Ile Leu 1180 1185	
	acg ctc agt gga acg aaa act cac gtt Thr Leu Ser Gly Thr Lys Thr His Val 1195 1200	
	tat caa aaa gga tct tca cct aga tcc yr Gln Lys Gly Ser Ser Pro Arg Ser 1210 1215	3694
~ -	tta aat caa tct aaa gta tat atg agt eu Asn Gln Ser Lys Val Tyr Met Ser 1230	3742
Lys Leu Gly Leu Thr Val Thr	aat gct taa tca gtg agg cac cta tct Asn Ala Ser Val Arg His Leu Ser 1245	3790
Gln Arg Ser Val Tyr Phe Val	cat cca tag ttg cct gac tcc ccg tcg His Pro Leu Pro Asp Ser Pro Ser 1255 1260	3838
	agg get tac cat ctg gcc cca gtg ctg arg Ala Tyr His Leu Ala Pro Val Leu 1270 1275	3886
caa tgataccgcg agacccacgc to Gln	accggete cagatttate agcaataaac	3939

cagecageeg gaagggeega gegeagaagt ggteetgeaa etttateege etecateeag 3999

```
tctattaatt qttqccqqqa aqctaqaqta aqtaqttcqc caqttaataq tttqcqcaac 4059
qttqttqcca ttqctqcaqq catcqtqqtq tcacqctcqt cqtttqqtat qqcttcattc 4119
ageteeggtt cecaacgate aaggegagtt acatgateee ceatgttgtg caaaaaageg 4179
gttageteet teggteetee gategttgte agaagtaagt tggcegeagt gttateacte 4239
atggttatgg cagcactgca taattetett actgtcatgc catccgtaag atgcttttet 4299
gtgactggtg agtactcaac caagtcattc tgagaatagt gtatgcggcg accgagttgc 4359
tettgeeegg egteaacaeg ggataataee gegeeacata geagaaettt aaaagtgete 4419
atcattggaa aacqttcttc ggggcgaaaa ctctcaagga tcttaccgct gttgagatcc 4479
agttegatgt aacceacteg tgcacceaac tgatetteag catettttac tttcaccage 4539
qtttctqqqt gaqcaaaaac aqqaagqcaa aatgccgcaa aaaaggqaat aagggcgaca 4599
cggaaatgtt gaatactcat actetteett tttcaatatt attgaagcat ttatcagggt 4659
tattgtctca tgageggata catatttgaa tgtatttaga aaaataaaca aataggggtt 4719
cogoquacat ttccccgaaa agtgccacct gacgtctaag aaaccattat tatcatgaca 4779
ttaacctata aaaataqqcq tatcacqaqq ccctttcgtc ttcaa
                                                                   4824
<210> 2
<211> 10
<212> PRT
<213> Salmonella typhimurium
Asn Ser Ile Pro Glu Leu Arg Val Ile Lys
                 5
<210> 3
<211> 7
<212> PRT
<213> Salmonella typhimurium
<400> 3
Arg Thr Gln Gln Phe Arg Tyr
 1
                 5
<210> 4
<211> 245
<212> PRT
<213> Artificial Sequence
<220>
<223> includes sequences from Salmonella typhimurium and
      Helicobacter pylori.
<400> 4
Ser Ser Thr Gly Glu Ile Ser Met Lys Leu Thr Pro Lys Glu Leu Asp
                 5
                                    10
Lys Leu Met Leu His Tyr Ala Gly Glu Leu Ala Lys Lys Arg Lys Glu
                                25
Lys Gly Ile Lys Leu Asn Tyr Val Glu Ala Val Ala Leu Ile Ser Ala
                             40
        35
```

His Ile Met Glu Glu Ala Arg Ala Gly Lys Lys Thr Ala Ala Glu Leu Met Gln Glu Gly Arg Thr Leu Leu Lys Pro Asp Asp Val Met Asp Gly 70 75 Val Ala Ser Met Ile His Glu Val Gly Ile Glu Ala Met Phe Pro Asp 90 Gly Thr Lys Leu Val Thr Val His Thr Pro Ile Glu Ala Asn Gly Lys 105 Leu Val Pro Gly Glu Leu Phe Leu Lys Asn Glu Asp Ile Thr Ile Asn 120 Glu Gly Lys Lys Ala Val Ser Val Lys Val Lys Asn Val Gly Asp Arg 135 Pro Val Gln Ile Gly Ser His Phe His Phe Phe Glu Val Asn Arg Cys Leu Asp Phe Asp Arg Glu Lys Thr Phe Gly Lys Arg Leu Asp Ile Ala 170 Ser Gly Thr Ala Val Arg Phe Glu Pro Gly Glu Glu Lys Ser Val Glu 185 Leu Ile Asp Ile Gly Gly Asn Arg Arg Ile Phe Gly Phe Asn Ala Leu 200 Val Asp Arg Gln Ala Asp Asn Glu Ser Lys Lys Ile Ala Leu His Arg 215 Ala Lys Glu Arg Gly Phe His Gly Ala Lys Ser Asp Asp Asn Tyr Val 230 Lys Thr Ile Lys Glu

<210> 5 <211> 570 <212> PRT

<213> Helicobacter pylori

	130					135					140				
Gln	Ile	Pro	Thr	Ala	Phe	Ala	ser	Gly	Val	Thr	Thr	Met	Ile	Gly	Gly
145					150					155					160
Gly	Thr	Gly	Pro		Asp	Gly	Thr	Asn		Thr	Thr	Ile	Thr		Gly
_	_	_	_	165	_		_	_	170				_	175	
Arg	Arg	Asn		Lys	Trp	Met	Leu		Ala	Ala	Glu	Glu		Ser	Met
	_		180	_	_ •	_		185	_				190	_	_
		195					Gly 200					205			
Ala	Asp 210	Gln	Ile	Glu	Ala	Gly 215	Ala	Ile	Gly	Phe	Ala 220	Ile	His	Glu	Asp
Trp 225	Gly	Thr	Thr	Pro	Ser 230	Ala	Ile	Asn	His	Ala 235	Leu	Asp	Val	Ala	Asp 240
	Tvr	Asp	Val	Gln		Ala	Ile	Ala	Thr		Thr	Leu	Asn	Glu	
-1-	-1-			245					250	E				255	
Gly	Cys	Val	Glu 260	Asp	Thr	Met	Ala	Ala 265		Ala	Gly	Arg	Thr 270		His
Thr	Phe	His		Glu	Glv	Ala	Gly		Glv	His	Ala	Pro		Ile	Ile
		275			•		280	-	_			285	•		
Lys	Val	Ala	Gly	Glu	His	Asn	Ile	Leu	Pro	Ala	Ser	Thr	Asn	Pro	Thr
	290					295					300				
Ile	Pro	Phe	Thr	Val	Asn	Thr	Glu	Ala	Glu	His	Met	Asp	Met	Leu	Met
305					310					315					320
Val	Cys	His	His	Leu	Asp	Lys	Ser	Ile	Lys	Glu	Asp	Val	Gln	Phe	Ala
				325					330					335	
Asp	Ser	Arg		Arg	Pro	Gln	Thr		Ala	Ala	Glu	Asp		Leu	His
		_	340					345	_		_		350		
Asp	Met	-	IIe	Phe	Ser	He	Thr	Ser	Ser	Asp	Ser		Ala	Met	Gly
7	3703	355	~1	val	r16	The	360	mb w	Tress	41 n	mbac	365	7.00	T ***	7 an
Arg	370	GIY	GIU	Vall	TIG	375	Arg	1111	тгр	GIII	380	Ala	Asp	ьуѕ	ASII
Larc		Glu	Dho	Clv) T.C.		Lys	Glu	Glu	Taze		λen	λen	7 en	λcn
385	БУБ	Giu	FIIC	GLY	390	ысц	пyъ	GIU	Gru	395	GLY.	nsp	ASII	тор	400
	Ara	Tle	Lvs	Ara		Leu	Ser	Lvs	Tvr		Ile	Asn	Pro	Ala	
	3		1	405	-1-			-1-	410				-,	415	
Ala	His	Gly	Ile	Ser	Glu	Tyr	Val	Gly		Val	Glu	Val	Gly	Lys	Val.
		-	420					425					430	-	
Ala	Asp	Leu	Val	Leu	Trp	ser	Pro	Ala	Phe	Phe	Gly	Val	Lys	Pro	Asn
		435					440					445			
Met	Ile	Ile	Lys	Gly	Gly	Phe	Ile	Ala	Leu	Ser	Gln	Met	Gly	Asp	Ala
	450					455					460				
Asn	Ala	Ser	Ile	Pro	Thr	Pro	Gln	Pro	Val	Tyr	Tyr	Arg	Glu	Met	Phe
465					470					475					480
Ala	His	His	Gly	Lys 485	Ala	ГÀг	Tyr	Asp	Ala 490	Asn	Ile	Thr	Phe	Val 495	Ser
Gln	Ala	Ala	Tyr	Asp	Lys	Gly	Ile	Lys	Glu	Glu	Leu	Gly	Leu	Glu	Arg
			500					505					510		
Gln	Val	Leu	Pro	Val	Lys	Asn	Cys	Arg	Asn	Ile	Thr	Lys	Lys	Asp	Met
		515					520					525			
Gln	Phe	Asn	Asp	Thr	Thr	Ala	His	Ile	Glu	Va1	Asn	Pro	Glu	Thr	Tyr
	530					535					540				

```
His Val Phe Val Asp Gly Lys Glu Val Thr Ser Lys Pro Ala Asn Lys
                    550
                                        555
Val Ser Leu Ala Gln Leu Phe Ser Ile Phe
                565
<210> 6
<211> 59
<212> PRT
<213> Salmonella typhimurium
<400> 6
Asp Phe Leu Gly Ala Thr Leu Leu Arg Ser Pro Gly Ile Gly Asp Pro
1
                5
                                   10
Leu Ala Arg Leu Met Ser Gly Leu Phe Phe Leu Gly Gln Arg Trp Val
Leu Ala Thr Gly Ala His Asp Arg Ala Pro Val Val Glu Asp Pro Ala
                           40
Arg Leu Ala Gly Leu Pro Tyr Trp Leu Ala Glu
<210> 7
<211> 67
<212> PRT
<213> Salmonella typhimurium
<400> 7
Ile Thr Asp Thr Arg Ala Asn Val Lys Arg Leu Leu Gln Asn Val
Cys Asp Leu Ser Asn Asn Met Asn Gly Leu Arg Phe Pro Cys Phe Val
Lys Ser Gly Asn Ala Glu Val Ser Ala Leu Pro Leu Pro Arg Ser Leu
                           40
Thr Arg Cys Ala Arg Ser Phe Gly Cys Gly Glu Arg Tyr Gln Leu Thr
                        55
Gln Arg Arg
<210> 8
<211> 141
<212> PRT
<213> Salmonella typhimurium
Tyr Gly Tyr Pro Gln Asn Gln Gly Ile Thr Gln Glu Arg Thr Cys Glu
1
                                   10
Gln Lys Ala Ser Lys Arg Pro Gly Thr Val Lys Arg Pro Arg Cys Trp
```

Arg Phe Ser Ile Gly Ser Ala Pro Leu Thr Ser Ile Thr Lys Ile Asp

```
35
                            40
Ala Gln Val Arg Gly Gly Glu Thr Arg Gln Asp Tyr Lys Asp Thr Arg
                        55
Arg Phe Pro Leu Glu Ala Pro Ser Cys Ala Leu Leu Phe Arg Pro Cys
                   70
                                        75
Arg Leu Pro Asp Thr Cys Pro Pro Phe Ser Leu Arg Glu Ala Trp Arg
                                    90
Phe Leu Asn Ala His Ala Val Gly Ile Ser Val Arg Cys Arg Ser Phe
                               . 105
Ala Pro Ser Trp Ala Val Cys Thr Asn Pro Pro Phe Ser Pro Thr Ala
                           120
Ala Pro Tyr Pro Val Thr Ile Val Leu Ser Pro Thr Arg
<210> 9
<211> 20
<212> PRT
<213> Salmonella typhimurium
<400> 9
Asp Thr Thr Tyr Arg His Trp Gln Gln Pro Leu Val Thr Gly Leu Ala
1
Glu Arg Gly Met
<210> 10
<211> 6
<212> PRT
<213> Salmonella typhimurium
<400> 10
Ala Val Leu Gln Ser Ser
<210> 11
<211> 19
<212> PRT
<213> Salmonella typhimurium
<400> 11
Ser Gly Gly Leu Thr Thr Ala Thr Leu Glu Gly Gln Tyr Leu Val Ser
                5
Ala Leu Cys
<210> 12
<211> 43
```

```
<212> PRT
<213> Salmonella typhimurium
<400> 12
Ser Gln Leu Pro Ser Glu Lys Glu Leu Val Ala Leu Asp Pro Ala Asn
                5
                                   10
Lys Pro Pro Leu Val Ala Val Val Phe Leu Phe Ala Ser Ser Arg Leu
Arg Ala Glu Lys Lys Asp Leu Lys Lys Ile Leu
<210> 13
<211> 20
<212> PRT
<213> Salmonella typhimurium
<400> 13
Ser Phe Leu Arg Gly Leu Thr Leu Ser Gly Thr Lys Thr His Val Lys
1
                                   10
Gly Phe Trp Ser
<210> 14
<211> 11
<212> PRT
<213> Salmonella typhimurium
<400> 14
Asp Tyr Gln Lys Gly Ser Ser Pro Arg Ser Phe
<210> 15
<211> 23
<212> PRT
<213> Salmonella typhimurium
<400> 15
Ile Lys Asn Glu Val Leu Asn Gln Ser Lys Val Tyr Met Ser Lys Leu
                5
                                   10
Gly Leu Thr Val Thr Asn Ala
            20
<210> 16
<211> 15
<212> PRT
<213> Salmonella typhimurium
```

```
<400> 16
Ser Val Arg His Leu Ser Gln Arg Ser Val Tyr Phe Val His Pro
                    10
<210> 17
<211> 8
<212> PRT
<213> Salmonella typhimurium
<400> 17
Leu Pro Asp Ser Pro Ser Cys Arg
<210> 18
<211> 14
<212> PRT
<213> Escherichia coli
<400> 18
Leu Arg Tyr Gly Arg Ala Tyr His Leu Ala Pro Val Leu Gln
          5
<210> 19
<211> 4824
<212> DNA
<213> Artificial Sequence
<220>
<223> includes sequences from Helicobacter pylori,
      Salmonella typhimurium, and Escherichia coli
<221> CDS
<222> (3893)...(3934)
<221> CDS
<222> (3938)...(4027)
<221> CDS
<222> (4031) ... (4285)
<221> CDS
<222> (4289)...(4300)
<221> CDS
<222> (4304) ... (4408)
<221> CDS
<222> (4412)...(4471)
```

<221> CDS

```
<222> (4475)...(4588)
<221> CDS
<222> (4592)...(4669)
<221> CDS
<222> (4673)...(4711)
<221> CDS
<222> (4715)...(4774)
<221> CDS
<222> (4784)...(4824)
<400> 19
quattetatt ccggaacttc gcgttataaa atgaatctga cgtacacagc aatttagata 60
ttaatcatcc acaggagaga tctccatgaa actcacccca aaagagttag ataagttgat 120
gctccactac gctggagaat tggctaaaaa acgcaaagaa aaaggcatta agcttaacta 180
tgtagaagca gtagctttga ttagtgccca tattatggaa gaagcgagag ctggtaaaaa 240
gactgegget gaattgatge aagaagggeg cactetttta aaaccagatg atgtgatgga 300
tggcgtggca agcatgatcc atgaagtggg tattgaagcg atgtttcctg atgggactaa 360
actcgtaacc gtgcataccc ctattgaggc caatggtaaa ttagttcctg gtgagttgtt 420
cttaaaaaat qaagacatca ctatcaacga aggcaaaaaa geegttageg tgaaagttaa 480
aaatgttggc gacagaccgg ttcaaatcgg ctcacacttc catttctttg aagtgaatag 540
atgcctagac tttgacagag aaaaaacttt cggtaaacgc ttagacattg cgagcgggac 600
ageggtaaga tttgageetg gegaagaaaa ateegtagaa ttgattgaca ttggeggtaa 660
cagaagaatc tttggattta acgcattggt tgatagacaa gcagacaacg aaagcaaaaa 720
aattgettta cacagageta aagagegtgg ttttcatgge getaaaageg atgacaacta 780
tgtaaaaaca attaaggagt aagaaatgaa aaagattagc agaaaagaat atgtttctat 840
qtatqqtcct actacaggcg ataaagtgag attgggcgat acagacttga tcgctgaagt 900
aqaacatqac tacaccattt atqqcqaaqa qcttaaattc gqtqqcqqta aaaccctaag 960
agaaggcatg agccaatcta acaaccctag caaagaagag ttggatttaa ttatcactaa 1020
cgctttaatc gtggattaca ccggtattta taaagcggat attggtatta aagatggcaa 1080
aatcgctggc attggtaaag gcggtaacaa agacatgcaa gatggcgtta aaaacaatct 1140
tagcgtaggt cetgetactg aagcettage eggtgaaggt ttgategtaa eggetggtgg 1200
tattgacaca cacatecact teattteace ceaacaaate cetacagett ttgcaagegg 1260
tqtaacaacc atgattggtg gtggaaccgg tcctgctgat ggcactaatg cgactactat 1320
cactccaggc agaagaaatt taaaatggat gctcagagcg gctgaagaat attctatgaa 1380
tttagqtttc ttggctaaag gtaacgcttc taacgatgcg agcttagccg atcaaattga 1440
agcoggtgcg attggctttg caattcacga agactggggc accactcctt ctgcaatcaa 1500
tcatgcgtta gatgttgcgg acaaatacga tgtgcaagtc gctatcgcca cagacacttt 1560
gaatgaagee ggttgtgtag aagaeactat ggetgetatt getggaegea etatgeacae 1620
tttccacact gaaggcgctg gcggcggaca cgctcctgat attattaaag tagccggtga 1680
acacaacatt cttcccqctt ccactaaccc caccatccct ttcaccqtga atacagaagc 1740
agageacatq gacatgetta tggtgtgeca ccaettggat aaaageatta aagaagatgt 1800
tcagttcgct gattcaagga tccgccctca aaccattgcg gctgaagaca ctttgcatga 1860
catggggatt tteteaatea ceagttetga eteteaageg atgggeegtg tgggtgaagt 1920
tatcactaga acttggcaaa cagctgacaa aaacaagaaa gaatttggcc gcttgaaaga 1980
agaaaaaaggc gataacgaca acttcaggat caaacgctac ttgtctaaat acaccattaa 2040
cccaqcqatc qctcatqqga ttagcgaqta tqtaggttca gtagaagtgg gcaaagtggc 2100
```

	cagcattett t	taacataaaa	cccaacatga tcatcaaagg	2160
cggattcatt gcgttaagcc				
ggtttattac agagaaatgt				
ttttgtgtct caagcggctt	_			
agtgttgccg gtaaaaaatt				
taccgctcac attgaagtca				
aacttctaaa ccagccaata				
tttaggagca acgctcctta				
cgggcttttt tttctcgggc				
tgtcgttgag gacccggcta				
cgatacgcga gcgaacgtga				
catgaatggt cttcggtttc				
tecgetteet egeteactga				
gctcactcaa aggcggtaat				
atgtgagcaa aaggccagca				
ttccataggc tccgccccc				
cgaaacccga caggactata				
tetectgtte egaceetgee				
gtggcgcttt ctcaatgctc				
aagctgggct gtgtgcacga				
tategtettg agtecaacce				
aacaggatta gcagagcgag				
aactacggct acactagaag	gedegedgge ;	ggtgttatag	ctctgctgaa gcgagttace	3480
ttcggaaaaa gagttggtag				
ttttttgttt gcaagcagca				
atcttttcta cggggtctga				
atgagattat caaaaaggat				
tcaatctaaa gtatatatga				
gcacctatct cagcgatctg				
tagataacta cgatacggga				
cagacaacta cgacacggga	gggcccacca	coaggeeea	Tyr Arg	
		*	1	,
			_	
gag acc cac gct cac c	ad ctc cad a	tt tat cad	caa taa acc agc cag	3946
gag acc cac gct cac c				3946
Glu Thr His Ala His A	rg Leu Gln I		Gln Thr Ser Gln	3946
				3946
Glu Thr His Ala His A 5	rg Leu Gln I	le Tyr Gln	Gln Thr Ser Gln 15	
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g	rg Leu Gln II 10 ca gaa gtg g	le Tyr Gln	Gln Thr Ser Gln 15 ctt tat ccg cct cca	3946 3994
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A	rg Leu Gln I 10 ca gaa gtg g la Glu Val V	le Tyr Gln	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro	
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g	rg Leu Gln II 10 ca gaa gtg g	le Tyr Gln	Gln Thr Ser Gln 15 ctt tat ccg cct cca	
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25	le Tyr Gln tc ctg caa al Leu Gln	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30	3994
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25 tt gcc ggg a	le Tyr Gln tc ctg caa al Leu Gln ag cta gag	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag	
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V	rg Leu Gln I 10 ca gaa gtg g la Glu Val Va 25 tt gcc ggg aa al Ala Gly L	le Tyr Gln tc ctg caa al Leu Gln ag cta gag	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln	3994
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25 tt gcc ggg a	le Tyr Gln tc ctg caa al Leu Gln ag cta gag	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag	3994
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35	rg Leu Gln I 10 ca gaa gtg g la Glu Val Va 25 tt gcc ggg aa al Ala Gly L	tc ctg caa al Leu Gln ag cta gag ys Leu Glu	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45	3994 4042
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35 tta ata gtt tgc gca a	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25 tt gcc ggg a al Ala Gly L 40 cg ttg ttg cc	tc ctg caa al Leu Gln ag cta gag ys Leu Glu	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45 cag gca tcg tgg tgt	3994
Glu Thr His Ala His A 5 Ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35 tta ata gtt tgc gca a Leu Ile Val Cys Ala T	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25 tt gcc ggg a al Ala Gly L 40 cg ttg ttg cc hr Leu Leu P	tc ctg caa al Leu Gln ag cta gag ys Leu Glu	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45 cag gca tcg tgg tgt Gln Ala Ser Trp Cys	3994 4042
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35 tta ata gtt tgc gca a	rg Leu Gln I 10 ca gaa gtg g la Glu Val V 25 tt gcc ggg a al Ala Gly L 40 cg ttg ttg cc	tc ctg caa al Leu Gln ag cta gag ys Leu Glu	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45 cag gca tcg tgg tgt	3994 4042
Glu Thr His Ala His A 5 ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35 tta ata gtt tgc gca a Leu Ile Val Cys Ala T 50	rg Leu Gln I 10 ca gaa gtg g la Glu Val Va 25 tt gcc ggg aa al Ala Gly Ly 40 cg ttg ttg ce hr Leu Leu P:	tc ctg caa al Leu Gln ag cta gag ys Leu Glu ca ttg ctg ro Leu Leu	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45 cag gca tcg tgg tgt Gln Ala Ser Trp Cys 60	3994 4042 4090
Glu Thr His Ala His A 5 Ccg gaa ggg ccg agc g Pro Glu Gly Pro Ser A 20 tcc agt cta tta att g Ser Ser Leu Leu Ile V 35 tta ata gtt tgc gca a Leu Ile Val Cys Ala T	rg Leu Gln I 10 ca gaa gtg g la Glu Val Va 25 tt gcc ggg aa al Ala Gly Ly 40 cg ttg ttg ce 55 ta tgg ctt ca	tc ctg caa al Leu Gln ag cta gag ys Leu Glu ca ttg ctg ro Leu Leu at tca gct	Gln Thr Ser Gln 15 ctt tat ccg cct cca Leu Tyr Pro Pro Pro 30 taa gta gtt cgc cag Val Val Arg Gln 45 cag gca tcg tgg tgt Gln Ala Ser Trp Cys 60 ccg gtt ccc aac gat	3994 4042

65					70					75					80	
				_	_			-	_	gca Ala		_			gct Ala	4186
	_			_	_	_		_	-	agt Ser		_	-	-		4234
					_					ctc Leu						4282
ccg Pro	P						eu Va			act hr Gl		ro Se				4330
										ctt Leu						4378
			ccg Pro							taa 1	ys (tca Ser S			4426
										gga Gly						4471
tga	_		_	_	_					cac His			_		-	4519
				•				_		gag Glu			_	•		4567
		_								cac His (4615
						Asn			_	gca Ala 245				_		4663
_	tca Ser	_	-	Asp					Val	ttt Phe 1 260			_	Asn 1		4711
tag	3 33	ttc	cgc	gca	cat	tțc	ccc	gaa	aag	tgc	cac	ctg	acg	tct	aag	4759

Gly Phe Arg Ala His Phe Pro Glu Lys Cys His Leu Thr Ser Lys 270 275 280

aaa cca tta tta tca tgacattaa cct ata aaa ata ggc gta tca cga ggc 4810 Lys Pro Leu Leu Ser Pro Ile Lys Ile Gly Val Ser Arg Gly 285

cct ttc gtc ttc aa Pro Phe Val Phe 4824

<210> 20

295

<211> 14

<212> PRT

<213> Escherichia coli

<400> 20

Tyr Arg Glu Thr His Ala His Arg Leu Gln Ile Tyr Gln Gln

<210> 21

<211> 30

<212> PRT

<213> Escherichia coli

<400> 21

Thr Ser Gln Pro Glu Gly Pro Ser Ala Glu Val Val Leu Gln Leu Tyr

1 5 10 15

Pro Pro Pro Ser Ser Leu Leu Ile Val Ala Gly Lys Leu Glu

20 25 30

<210> 22

<211> 85

<212> PRT

<213> Escherichia coli

<400> 22

Val Val Arg Gln Leu Ile Val Cys Ala Thr Leu Leu Pro Leu Leu Gln
1 5 10 15

Ala Ser Trp Cys His Ala Arg Arg Leu Val Trp Leu His Ser Ala Pro 20 25 30

Val Pro Asn Asp Gln Gly Glu Leu His Asp Pro Pro Cys Cys Ala Lys

Lys Arg Leu Ala Pro Ser Val Leu Arg Ser Leu Ser Glu Val Ser Trp 50 55 60

Pro Gln Cys Tyr His Ser Trp Leu Trp Gln His Cys Ile Ile Leu Leu 65 70 75 80

Leu Ser Cys His Pro

85

```
<210> 23
<211> 4
<212> PRT
<213> Escherichia coli
<400> 23
Asp Ala Phe Leu
1
<210> 24
<211> 35
<212> PRT
<213> Escherichia coli
<400> 24
Leu Val Ser Thr Gln Pro Ser His Ser Glu Asn Ser Val Cys Gly Asp
1
              5
                                10
                                                   15
Arg Val Ala Leu Ala Arg Arg Cln His Gly Ile Ile Pro Arg His Ile
                             25
Ala Glu Leu
35
<210> 25
<211> 20
<212> PRT
<213> Escherichia coli
Lys Cys Ser Ser Leu Glu Asn Val Leu Arg Gly Glu Asn Ser Gln Gly
1
                                 10
Ser Tyr Arg Cys
           20
<210> 26
<211> 38
<212> PRT
<213> Escherichia coli
<400> 26
Asp Pro Val Arg Cys Asn Pro Leu Val His Pro Thr Asp Leu Gln His
1 5
                                 10
Leu Leu Ser Pro Ala Phe Leu Gly Glu Gln Lys Gln Glu Gly Lys
           20
                             25
Met Pro Gln Lys Arg Glu
       35
```

```
<210> 27
<211> 26
<212> PRT
<213> Escherichia coli
<400> 27
Gly Arg His Gly Asn Val Glu Tyr Ser Tyr Ser Ser Phe Phe Asn Ile
                        10
               5
Ile Glu Ala Phe Ile Arg Val Ile Val Ser
  . 20
<210> 28
<211> 13
<212> PRT
<213> Escherichia coli
<400> 28
Ala Asp Thr Tyr Leu Asn Val Phe Arg Lys Ile Asn Lys
<210> 29
<211> 20
<212> PRT
<213> Salmonella typhimurium
Gly Phe Arg Ala His Phe Pro Glu Lys Cys His Leu Thr Ser Lys Lys
1
                               10
Pro Leu Leu Ser
            20
<210> 30
<211> 13
<212> PRT
<213> Salmonella typhimurium
Pro Ile Lys Ile Gly Val Ser Arg Gly Pro Phe Val Phe
                5
<210> 31
<211> 31
<212> DNA
<213> Helicobacter pylori
<400> 31
```

•		
tagggaattc tcatgaaact caccccaaaa g		31
<210> 32		
<211> 22		
<212> DNA		
<213> Helicobacter pylori		
distribution principle		
<400> 32		
gccaacttag cttcctttcg gg		22
<210> 33	•	
<211> 34		
<212> DNA		
<213> Helicobacter pylori		
.400- 22		
<400> 33		34
tctactgcag gatccaaaat gctaaagagt tgcg		34
<210> 34		
<211> 21		
<212> DNA		
<213> Salmonella typhimurium		
CEED, Burmondra Official		
<400> 34		
tcaaatggta ccccttgctg a		21
<210> 35		
<211> 20		
<212> DNA		
<213> Salmonella typhimurium		
.400. 25		
<400> 35		20
tattccggaa cttcgcgtta		20
<210> 36		
<211> 23		
<212> DNA		
<213> Helicobacter pylori		
1210) Nettoobacoti pytoti		
<400> 36		
tgtttcctga tgggactaaa ctc		23
• • • • • • • • • • • • • • • • • • • •		
<210> 37	·	
<211> 22		
<212> DNA		
<213> Helicobacter pylori		
•		
<400> 37		
accaggaact aatttaccat tg		22
<210> 38		

PCT/US00/30191

WO 01/32014

<211> 21	
<212> DNA	
<213> Helicobacter pylori	
<400> 38	
ttgattgaca ttggcggtaa c	21
-210- 20	
<210> 39	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	
<400> 39	~ ~
gttgtctgct tgtctatcaa cc	22
210 40	
<210> 40	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	
<400> 40	
ggtggcggta aaaccctaag ag	22
<210> 41	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	
<400> 41	
ctttgctagg gttgttagat tg	22
<210> 42	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	
,	
<400> 42	
aatccctaca gcttttgcaa gc	22
<210> 43	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	
<400> 43	
gtgccatcag caggaccggt tc	22
<210> 44	
<211> 22	
<212> DNA	
<213> Helicobacter pylori	

PCT/US00/30191

WO 01/32014

•		
<400> 44		
atcgccacag acactttgaa tg		22
acceptance acceptance		22
<210> 45		
<211> 22		
<212> DNA		
<213> Helicobacter pylori		
(213) hericobaccer pyrori		
<400> 45	•	
tagcagecat agtgtettet ac	•	22
cageagecae agegeeecee ac	<u>~</u>	22
<210> 46		
<211> 22		
<212> DNA		
·		
<213> Helicobacter pylori		
<400> 46		
		22
tgaagacact ttgcatgaca tg		22
<210> 47	1	
<211> 47		
<211> 22 <212> DNA	,	
<213> Helicobacter pylori	·	
<400> 47		
tgagagtcag aactggtgat tg		22
egugugeeug udeeggegue eg		22
<210> 48		
<211> 22		
<212> DNA		
<213> Helicobacter pylori	·	
verso herreobacter pyrorr		
<400> 48		
catgatcatc aaaggcggat to		22
anguesas anggeggas ce		~ ~
<210> 49		
<211> 23		
<212> DNA		
<213> Helicobacter pylori		
, managed by total		
<400> 49		
gaagcgttcg catcgcccat ttg	·	23
J		
<210> 50		
<211> 22	•	
<212> DNA		
<213> Helicobacter pylori		
The Manager Plant		
<400> 50		
tegtagatag caaagaagta ac		22

PCT/US00/30191

WO 01/32014

<210> 51	
<211> 20	
<212> DNA	
<213> Helicobacter pylori	
<400> 51	
gcgccaagct cactttattg	20
3030000300 3	
<210> 52	
<211> 22	
<212> DNA	
<213> Salmonella typhimurium	
<400> 52	ງ ງ
caacgacagg agcacgatca tg	22

-25*-*